GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 23:19:15 ; Search time 4188 Seconds
(without alignments)
16601.386 Million cell updates/sec

Title: US-08-961-083-55
Perfect score: 2389
Sequence: 1 TTCTTACGAGTTGGGACTGT.....TAAGTAAGGAAAAAATAAAC 2389

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		2388	100.0	2389	6	AR120265	AR120265 Sequence
2		2388	100.0	2541	1	AF291695	AF291695 Streptoco
3		2388	100.0	8195	6	BD003774	BD003774 Polynucle
4	c	2388	100.0	10256	1	AE007418	AE007418 Streptoco
5	c	2365.6	99.0	10320	1	AE008479	AE008479 Streptoco
6		2328.2	97.5	20035	2	SPNEU1915	AL449937 Streptoco
7		1434.4	60.0	2535	1	AF340221	AF340221 Streptoco
8		1374.2	57.5	2523	6	AX343072	AX343072 Sequence
9		1374.2	57.5	2647	6	AX343073	AX343073 Sequence
10		991	41.5	2457	1	AF318954	AF318954 Streptoco
11		990	41.4	2517	1	AF318955	AF318955 Streptoco
12		990	41.4	11931	1	AE007403	AE007403 Streptoco
13		988.4	41.4	232807	2	SPNEU1901	AL449923 Streptoco
14		987.6	41.3	2290	6	AR120270	AR120270 Sequence
15		980.8	41.1	2639	6	AX343074	AX343074 Sequence
16		962.8	40.3	12372	1	AE008464	AE008464 Streptoco
17		869.4	36.4	2166	12	AF340222	AF340222 Synthetic
18	c	835.8	35.0	75874	2	SPNEU1907	AL449929 Streptoco
19		674	28.2	702	2	SPNEU1929	AL449951 Streptoco
20		653.8	27.4	2359	6	BD003923	BD003923 Polynucle
21		385.4	16.1	1342	6	AR120328	AR120328 Sequence
22		385.4	16.1	3120	1	AF318956	AF318956 Streptoco
23		385.4	16.1	3120	6	AX343070	AX343070 Sequence
24		385.4	16.1	5048	6	AX343071	AX343071 Sequence
25	c	385.4	16.1	6867	6	BD003872	BD003872 Polynucle
26		381.4	16.0	973	6	BD004035	BD004035 Polynucle
27		347	14.5	2528	6	AX343078	AX343078 Sequence
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38		188.2	7.9	492	12	AF340223	AF340223 Synthetic
39	c	109	4.6	841	6	AR089275	AR089275 Sequence
40	c	109	4.6	841	6	AR093475	AR093475 Sequence
41	c	70.6	3.0	115758	9	AC104634	AC104634 Homo sapi
42		63.4	2.7	170522	9	AP002387	AP002387 Homo sapi
43		60.2	2.5	51939	9	AC099341	AC099341 Homo sapi
44		60	2.5	61052	2	AC117074	AC117074 Dictyoste
45		60	2.5	61052	2	AC123513	AC123513 Dictyoste

ALIGNMENTS

RESULT 1
AR120265
LOCUS AR120265 2389 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 55 from patent US 6159469.
ACCESSION AR120265
VERSION AR120265.1 GI:14103841
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2389)
AUTHORS Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B., Fannon,M.R. and Rosen,C.A.
TITLE Streptococcus pneumoniae antigens and vaccines
JOURNAL Patent: US 6159469-A 55 12-DEC-2000;

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FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      830 a    461 c    486 g    611 t      1 others
ORIGIN
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Query Match 100.0%; Score 2388; DB 6; Length 2389;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040
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RESULT 2
AF291695
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DEFINITION Streptococcus pneumoniae pneumococcal histidine triad A protein (phtA) gene, complete cds.
ACCESSION AF291695
VERSION AF291695.1 GI:13345012
KEYWORDS .
SOURCE Streptococcus pneumoniae.
ORGANISM Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 2541)
AUTHORS Wizemann,T.M., Heinrichs,J.H., Adamou,J.E., Erwin,A.L., Kunsch,C., Choi,G.H., Barash,S.C., Rosen,C.A., Masure,H.R., Tuomanen,E., Gayle,A., Brewah,Y.A., Walsh,W., Barren,P., Lathigra,R., Hanson,M., Langermann,S., Johnson,S. and Koenig,S.
TITLE Use of a whole genome approach to identify vaccine molecules affording protection against Streptococcus pneumoniae infection
JOURNAL Infect. Immun. 69 (3), 1593-1598 (2001)
MEDLINE 21116976
PUBMED 11179332
REFERENCE 2 (bases 1 to 2541)
AUTHORS Choi,G.H.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2000) Molecular Biology, Human Genome Sciences, Inc., 9410 Key West Ave., Rockville, MD 20850, USA
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BASE COUNT 888 a 476 c 516 g 660 t 1 others
ORIGIN

Query Match 100.0%; Score 2388; DB 1; Length 2541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
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Qy    841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
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Qy   1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260
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Qy   1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560
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Qy   1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740
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Qy   1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800
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Qy   1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920
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Qy   1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040
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Qy   2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 2100
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Qy   2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280
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Qy   2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340
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DEFINITION  Polynucleotide of Streptococcus pneumoniae and sequence.
ACCESSION   BD003774
VERSION     BD003774.1  GI:18631735
KEYWORDS    JP 2001501833-A/94.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 8195)
  AUTHORS   Kunsch,C.A., Choi,G.H., Dillon,P.J., Rosen,C.A., Bara,S.C.,
            Fannon,M. and Dougherty,B.A.
  TITLE     Polynucleotide of Streptococcus pneumoniae and sequence
  JOURNAL   Patent: JP 2001501833-A 94 13-FEB-2001;
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COMMENT     OS   Unidentified
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            PD   13-FEB-2001
            PF   30-OCT-1997 JP 1998520718
            PR   31-OCT-1996 US    60/029960
            PI   CHARLES A KUNSCH,GIL H CHOI,PATRICK J DILLON,CRAIG A ROSEN, PI
              STEVEN C BARASH,
            PI   MICHAEL FANNON,BRIAN A DOUGHERTY
            PC   C12N15/09,A01K67/027,C07K14/315,C07K16/12,C12N1/15,C12N1/19,
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            PC   C12N5/10,C12P21/02,C12Q1/68,G06F17/30,C12N15/00,C12N5/00, PC
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  Best Local Similarity 100.0%;  Pred. No. 0;
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Db   3113 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 3172

Qy    121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
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Qy    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
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Qy    361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
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Db   3593 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 3652

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Db   3773 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 3832

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Qy    901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960
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Qy    961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
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Qy   1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080
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Qy    2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 2220
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RESULT 4
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DEFINITION  Streptococcus pneumoniae TIGR4  section 101 of 194 of the complete
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ACCESSION   AE007418 AE005672
VERSION     AE007418.1  GI:14972649
KEYWORDS    .
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REFERENCE   1  (bases 1 to 10256)
  AUTHORS   Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D.,
            Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J.,
            Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D.,
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            Fraser,C.M.
  TITLE     Complete genome sequence of a virulent isolate of Streptococcus
            pneumoniae
  JOURNAL   Science 293 (5529), 498-506 (2001)
  MEDLINE   21357209
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  AUTHORS   Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D.,
            Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J.,
            Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D.,
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            Loftus,B.J., Ujwal,M.L., Yang,F., Smith,H.O., Venter,J.C.,
            Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-2001) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
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  AUTHORS   Hoskins,J.A., Alborn,W. Jr., Arnold,J., Blaszczak,L., Burgett,S.,
            DeHoff,B.S., Estrem,S., Fritz,L., Fu,D.-J., Fuller,W., Geringer,C.,
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            and Glass,J.I.
  TITLE     Genome of the bacterium Streptococcus pneumoniae strain R6
  JOURNAL   J. Bacteriol. 183 (19), 5709-5717 (2001)
  MEDLINE   21429245
   PUBMED   11544234
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  AUTHORS   Hoskins,J.A., Alborn,W. Jr., Arnold,J., Blaszczak,L., Burgett,S.,
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  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUL-2001) Infectious Diseases Research, Eli Lilly and
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  AUTHORS   Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y.,
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            Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., Peitsch,M.
            and Garcia-Bustos,J.F.
  TITLE     Annotated draft genomic sequence from a Streptococcus pneumoniae
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  JOURNAL   Microb. Drug Resist. 7 (2), 99-125 (2001)
  MEDLINE   21335329
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            Francesco,M., Buell,G., Feger,G., Garcia,E., Peitsch,M. and
            Garcia-Bustos,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-OCT-2000) Research Department, Glaxo Wellcome, S.A.,
            Severo Ochoa 2, 28760 Tres Cantos, SPAIN
COMMENT     * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
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Db   17730 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 17789

Qy     721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   17790 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 17849

Qy     781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840
          |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   17850 ARCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 17909

Qy     841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
          ||||||:|||||||||||||||||||||| || || ||||| ||||||||||||||||||
Db   17910 TCAACGMCATGTAGAATCTGATGGCCTTGTTTTCGACCCAGCGCAAATCACAAGTCGAAC 17969

Qy     901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960
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Db   17970 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 18029

Qy     961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18030 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 18089

Qy    1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080
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Db   18090 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 18149

Qy    1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140
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Db   18150 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 18209

Qy    1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200
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Qy    1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260
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Db   18270 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 18329

Qy    1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
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Db   18330 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTW 18389

Qy    1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380
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Qy    1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGAC-TA 1439
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Qy    1440 ATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGC 1499
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Db   18510 ATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGC 18569

Qy    1500 GACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAAT 1559
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Qy   1560 TAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTG 1619
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Db  18630 TAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTG 18689

Qy   1620 ATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATA 1679
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Db  18690 ATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGACA 18749

Qy   1680 GCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTAC 1739
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Db  18750 GCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTAC 18809

Qy   1740 CTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTT 1799
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Qy   1800 ACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGC 1859
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Qy   1860 ATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATA 1919
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Db  18930 ATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAACA 18989

Qy   1920 TTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAG 1979
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Qy   1980 ATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATG 2039
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Db  19050 ATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATG 19109

Qy   2040 ATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAA 2099
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Db  19110 ATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAA 19169

Qy   2100 ATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCC 2159
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Db  19170 ATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCC 19229

Qy   2160 CTCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGA 2219
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Db  19230 CTCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGA 19289

Qy   2220 AAGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATA 2279
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Db  19290 AAGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATA 19349

Qy   2280 ATTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTG 2339
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Db  19350 ATTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTG 19409

Qy   2340 CGTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389
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RESULT 7
AF340221
LOCUS       AF340221               2535 bp    DNA     linear   BCT 22-MAY-2001
DEFINITION  Streptococcus pneumoniae PhpA (phpA) gene, complete cds.
ACCESSION   AF340221
VERSION     AF340221.1  GI:13447093
KEYWORDS    .
SOURCE      Streptococcus pneumoniae.
  ORGANISM  Streptococcus pneumoniae
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 2535)
  AUTHORS   Zhang,Y., Masi,A.W., Barniak,V., Mountzouros,K., Hostetter,M.K. and
            Green,B.A.
  TITLE     Recombinant PhpA protein, a unique histidine motif-containing
            protein from Streptococcus pneumoniae, protects mice against
            intranasal pneumococcal challenge
  JOURNAL   Infect. Immun. 69 (6), 3827-3836 (2001)
  MEDLINE   21246685
   PUBMED   11349048
REFERENCE   2  (bases 1 to 2535)
  AUTHORS   Zhang,Y., Masi,A., Barniak,V., Mountzouros,K., Hostetter,M. and
            Green,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JAN-2001) Department of Bacteriology, Wyeth Lederle
            Vaccines, 211 Bailey Road, West Henrietta, NY 14586, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:1313"
     gene            1. .2535
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                     ELSASELAAAKAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSN
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                     IPYSQLSPLEEKLARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSPQPAPNPQPAPS
                     NPIDEKLVKEAVRKVGDGYVFEENGVPRYIPAKDLSAETAAGIDSKLAKQESLSHKLG
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                     NRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSL
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                     EETPREEKPQSEKPESPKPTEEPEEESPEESPEESEEPQVETEKVKEKLREAEDLLGK
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BASE COUNT      880 a    518 c    533 g    604 t
ORIGIN
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Query Match 60.0%; Score 1434.4; DB 1; Length 2535;
Best Local Similarity 79.0%; Pred. No. 3.3e-296;
Matches 1724; Conservative 0; Mismatches 447; Indels 12; Gaps 1;

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Db     60 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 119

Qy     61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
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Qy    121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
          |||||||||||||||||  || ||||||||||||| ||||||||||||||||||||||||
Db    180 GCGTGAAGGAATCAATGCCGAACAAATCGTCATCAAAATAACAGACCAAGGCTATGTCAC 239

Qy    181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240
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Db    240 TTCACATGGGGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 299

Qy    241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300
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Db    300 TGAAGAATTGCTGATGAAGGATCCAAACTACCAGCTAAAGGACGAGGATATTATCAGTGA 359

Qy    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
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Db    360 AATCAAGGGTGGTTATGTGATTAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 419

Qy    361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
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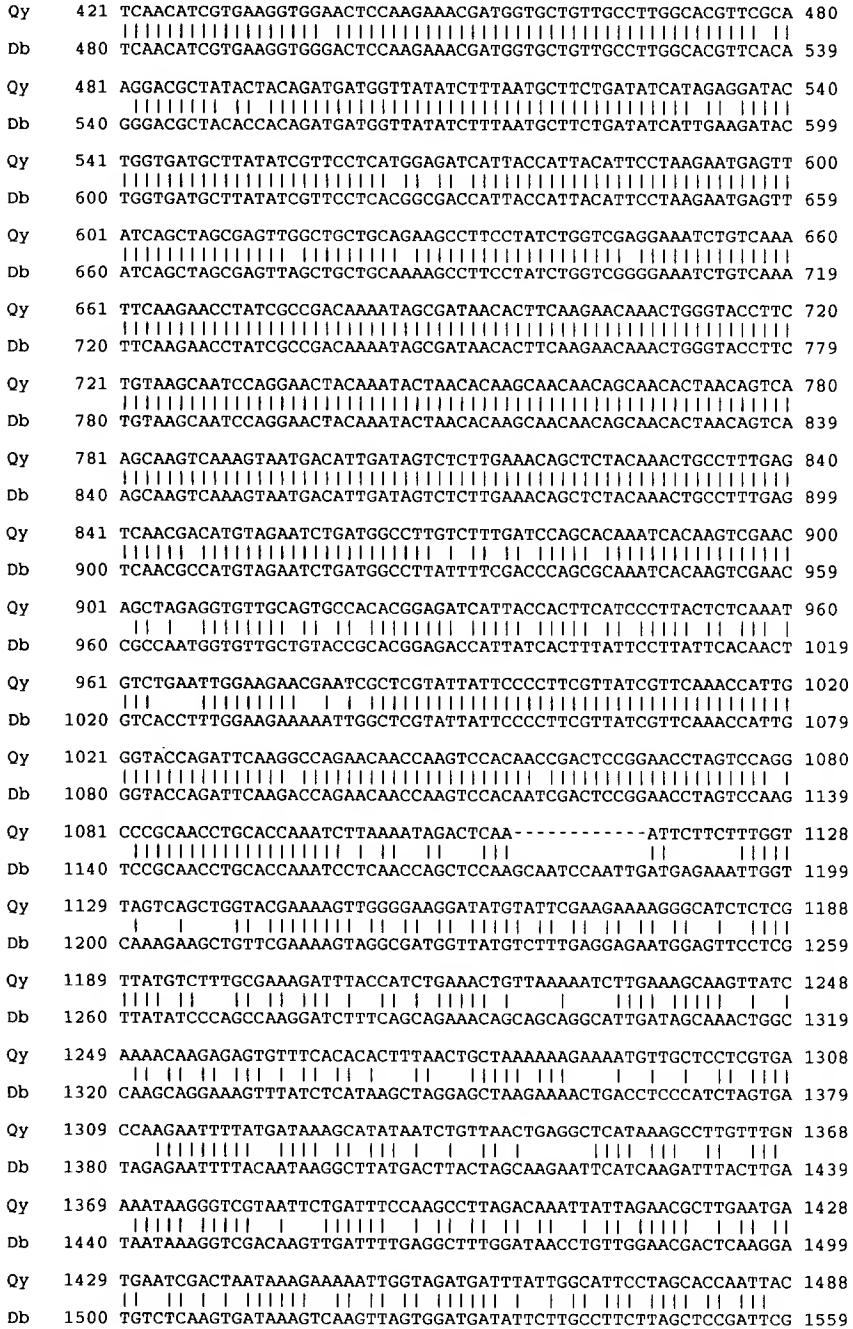

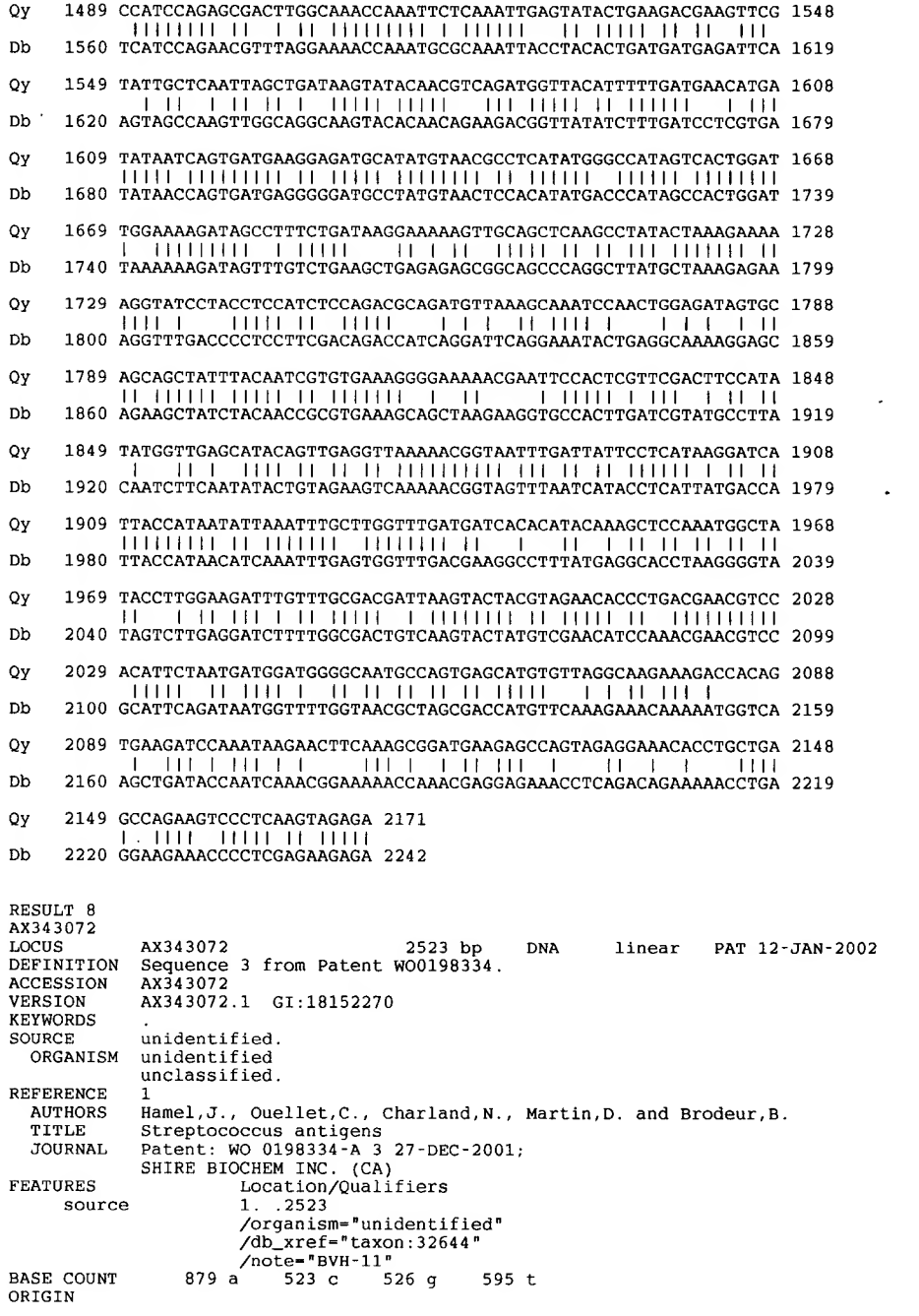

RESULT 8
AX343072
LOCUS AX343072 2523 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 3 from Patent WO0198334.
ACCESSION AX343072
VERSION AX343072.1 GI:18152270
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Hamel,J., Ouellet,C., Charland,N., Martin,D. and Brodeur,B.
TITLE Streptococcus antigens
JOURNAL Patent: WO 0198334-A 3 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
FEATURES Location/Qualifiers
source 1. .2523
/organism="unidentified"
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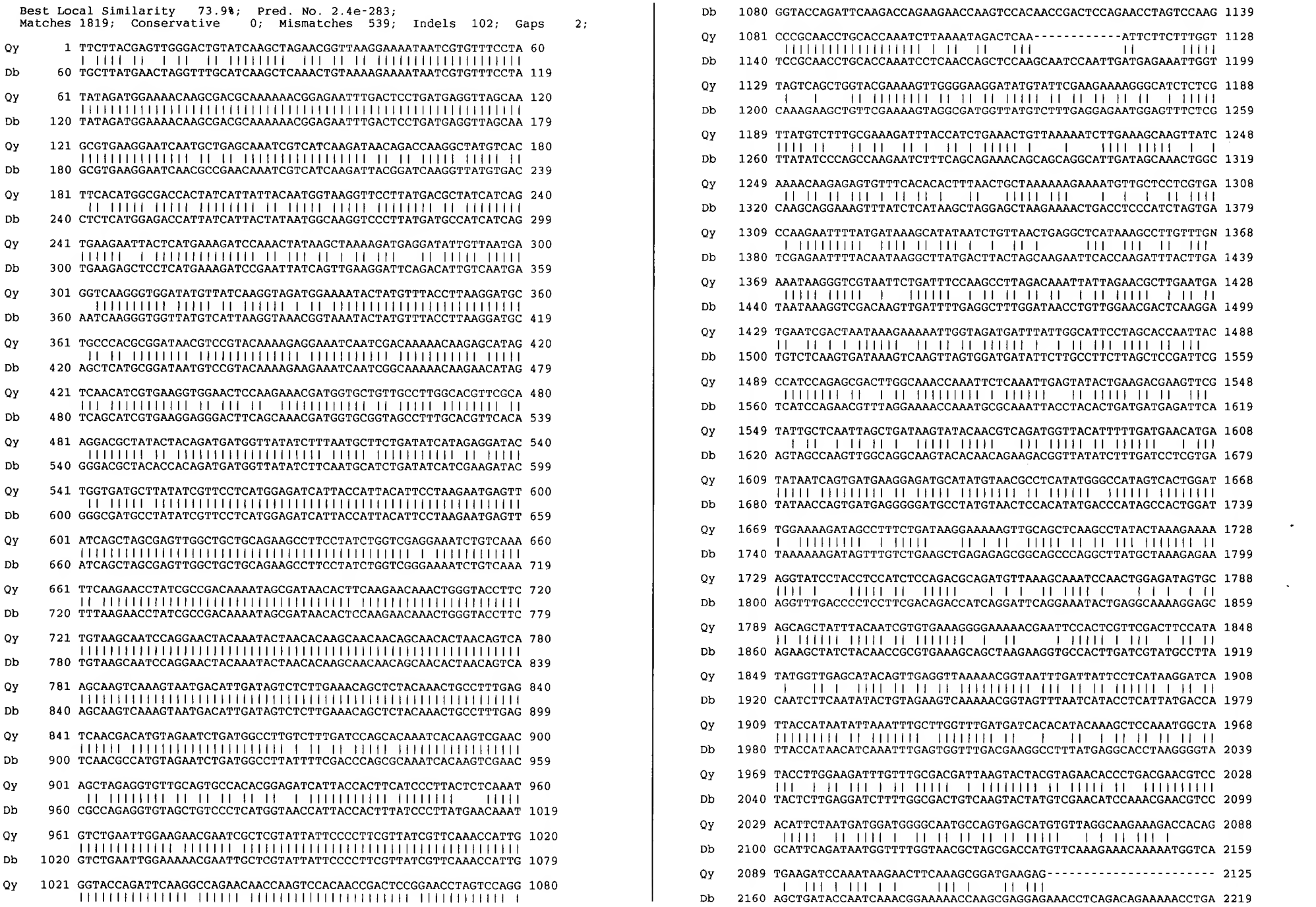
/note="BVH-11"
BASE COUNT 879 a 523 c 526 g 595 t
ORIGIN

Query Match 57.5%; Score 1374.2; DB 6; Length 2523;

Best Local Similarity 73.9%; Pred. No. 2.4e-283;
Matches 1819; Conservative 0; Mismatches 539; Indels 102; Gaps 2;



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Qy   2126 ------------------------------------------------------------ 2125

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Qy   2126 -------CCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA 2178
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Db   2280 AGAGGAACCAGAAGAAGAATCACCAGAGGAATCAGAAGAACCTCAGGTCGAGACTGAAAA 2339

Qy   2179 AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT 2238
           || ||||   |||| | ||| || |||| ||| ||||  ||| |   |||| | | | |
Db   2340 GGTTGAAGAAAAACTGAGAGAGGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTAT 2399

Qy   2239 GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT 2298
           ||  |||||||| | ||| |||||  | || |||  ||||||||     ||   |
Db   2400 CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA 2459

Qy   2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358
          ||| ||||||| ||| |||||||||| |||||| || | || || ||||| |  |||||
Db   2460 GGACAACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA 2519


RESULT 9
AX343073
LOCUS       AX343073               2647 bp    DNA     linear   PAT 12-JAN-2002
DEFINITION  Sequence 4 from Patent WO0198334.
ACCESSION   AX343073
VERSION     AX343073.1  GI:18152271
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Hamel,J., Ouellet,C., Charland,N., Martin,D. and Brodeur,B.
  TITLE     Streptococcus antigens
  JOURNAL   Patent: WO 0198334-A 4 27-DEC-2001;
            SHIRE BIOCHEM INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .2647
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ORIGIN

  Query Match             57.5%;  Score 1374.2;  DB 6;  Length 2647;
  Best Local Similarity   73.9%;  Pred. No. 2.4e-283;
  Matches 1819;  Conservative    0;  Mismatches  539;  Indels  102;  Gaps    2;

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Db    104 TGCTTATGAACTAGGTTTGCATCAAGCTCAAACTGTAAAAGAAAATAATCGTGTTTCCTA 163

Qy     61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
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Qy    121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
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Qy    181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240
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Qy    241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300
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Qy    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
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Db    404 AATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTTTACCTTAAGGATGC 463

Qy    361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
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Qy    421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480
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Db    524 TCAGCATCGTGAAGGAGGGACTTCAGCAAACGATGGTGCGGTAGCCTTTGCACGTTCACA 583

Qy    481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540
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Db    584 GGGACGCTACACCACAGATGATGGTTATATCTTCAATGCATCTGATATCATCGAAGATAC 643

Qy    541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600
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Db    644 GGGCGATGCCTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 703

Qy    601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660
          |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Db    704 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGGGAAAATCTGTCAAA 763

Qy    661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720
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Db    764 TTTAAGAACCTATCGCCGACAAAATAGCGATAACACTCCAAGAACAAACTGGGTACCTTC 823

Qy    721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780
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Db    824 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 883

Qy    781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840
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Qy    841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
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Qy    901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960
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Qy    961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
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Qy   1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080
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Db   1124 GGTACCAGATTCAAGACCAGAAGAACCAAGTCCACAACCGACTCCAGAACCTAGTCCAAG 1183

Qy   1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAA----------ATTCTTCTTTGGT 1128
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Db   1184 TCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATTGGT 1243

Qy   1129 TAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCG 1188
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Qy   1189 TTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATC 1248
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Db   1364 CAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAGTGA 1423

Qy   1309 CCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGN 1368
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Db   1424 TCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACTTGA 1483

Qy   1369 AAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGA 1428
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Qy    1969 TACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCC 2028
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RESULT 10
AF318954
LOCUS AF318954 2457 bp DNA linear BCT 11-FEB-2001
DEFINITION Streptococcus pneumoniae pneumococcal histidine triad protein B precursor (phtB) gene, partial cds.

ACCESSION AF318954
VERSION AF318954.1 GI:12744741
KEYWORDS .
SOURCE Streptococcus pneumoniae.
ORGANISM Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 2457)
AUTHORS Adamou,J.E., Heinrichs,J.H., Erwin,A.L., Walsh,W., Gayle,T., Dormitzer,M., Dagan,R., Brewah,Y.A., Barren,P., Lathigra,R., Langermann,S., Koenig,S. and Johnson,S.
TITLE Identification and characterization of a novel family of pneumococcal proteins that are protective against sepsis
JOURNAL Infect. Immun. 69 (2), 949-958 (2001)
MEDLINE 21101045
PUBMED 11159990
REFERENCE 2 (bases 1 to 2457)
AUTHORS Adamou,J.E., Heinrichs,J.H., Erwin,A.L., Walsh,W., Dormitzer,M. and Johnson,S.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) Molecular Microbiology, MedImmune, Inc., 35 West Watkins Mill Road, Gaithersburg, MD 20878, USA
FEATURES Location/Qualifiers

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Qy    238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297
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Qy    298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
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Qy    478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
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RESULT 11
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DEFINITION Streptococcus pneumoniae pneumococcal histidine triad protein D precursor (phtD) gene, partial cds.
ACCESSION AF318955
VERSION AF318955.1 GI:12744743
KEYWORDS .
SOURCE Streptococcus pneumoniae.
ORGANISM Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 2517)
AUTHORS Adamou,J.E., Heinrichs,J.H., Erwin,A.L., Walsh,W., Gayle,T., Dormitzer,M., Dagan,R., Brewah,Y.A., Barren,P., Lathigra,R., Langermann,S., Koenig,S. and Johnson,S.
TITLE Identification and characterization of a novel family of pneumococcal proteins that are protective against sepsis
JOURNAL Infect. Immun. 69 (2), 949-958 (2001)
MEDLINE 21101045
PUBMED 11159990
REFERENCE 2 (bases 1 to 2517)
AUTHORS Adamou,J.E., Heinrichs,J.H., Erwin,A.L., Walsh,W., Dormitzer,M. and Johnson,S.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) Molecular Microbiology, MedImmune, Inc., 35 West Watkins Mill Road, Gaithersburg, MD 20878, USA
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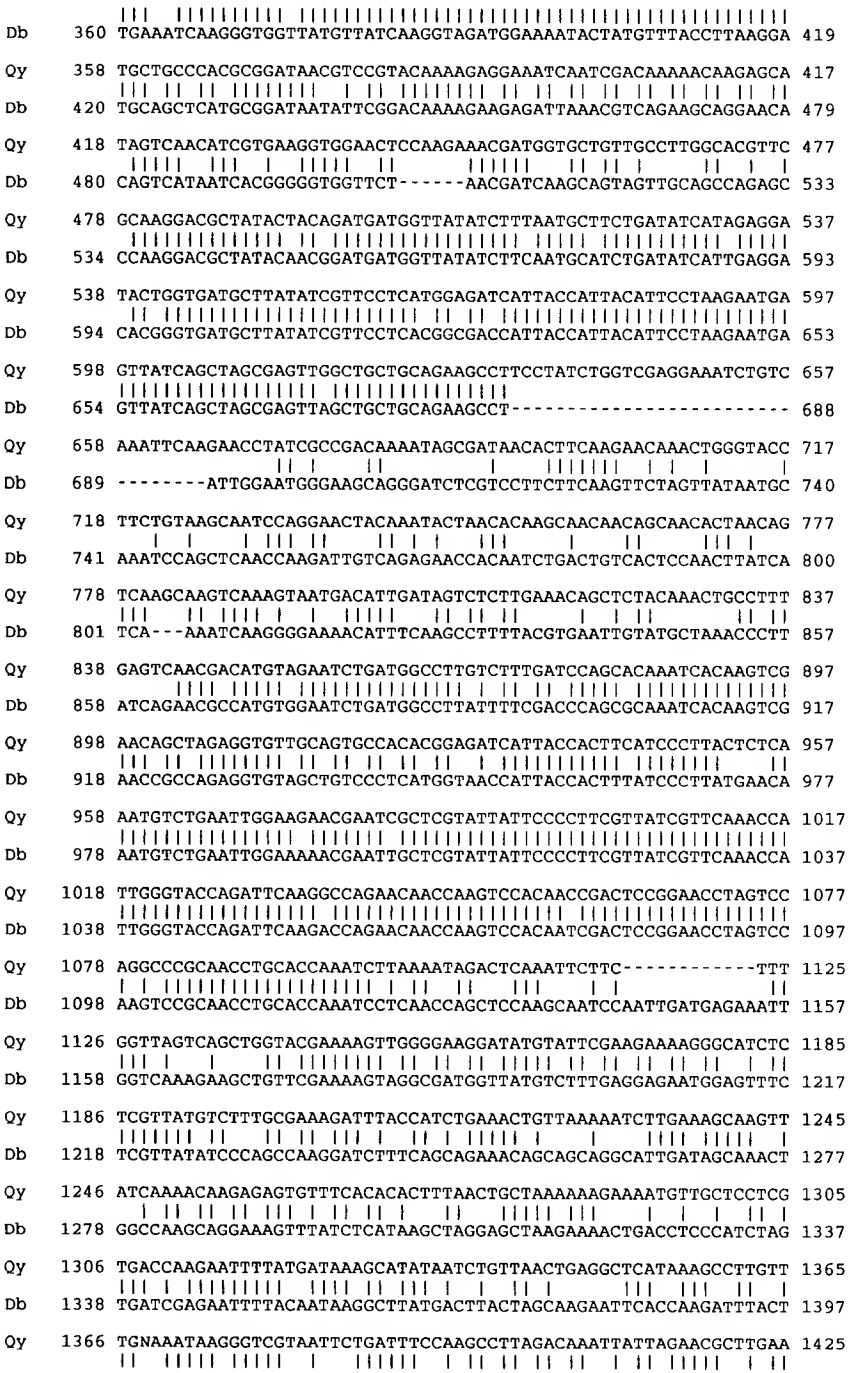

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DEFINITION Streptococcus pneumoniae TIGR4 section 86 of 194 of the complete genome.
ACCESSION AE007403 AE005672
VERSION AE007403.1 GI:14972469
KEYWORDS .
SOURCE Streptococcus pneumoniae TIGR4.
ORGANISM Streptococcus pneumoniae TIGR4
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 11931)
AUTHORS Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D., Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J., Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D., Umayam,L.A., White,O., Salzberg,S.L., Lewis,M.R., Radune,D., Holtzapple,E., Khouri,H., Wolf,A.M., Utterback,T.R., Hansen,C.L.,

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            McDonald,L.A., Feldblyum,T.V., Angiuoli,S., Dickinson,T.,
            Hickey,E.K., Holt,I.E., Loftus,B.J., Yang,F., Smith,H.O.,
            Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and
            Fraser,C.M.
  TITLE     Complete genome sequence of a virulent isolate of Streptococcus
            pneumoniae
  JOURNAL   Science 293 (5529), 498-506 (2001)
  MEDLINE   21357209
   PUBMED   11463916
REFERENCE   2  (bases 1 to 11931)
  AUTHORS   Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D.,
            Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J.,
            Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D.,
            Umayam,L.A., White,O., Lewis,M.R., Radune,D., Holtzapple,E.,
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            Feldblyum,T.V., Angiuoli,S., Gesuwan,P., Hickey,E.K., Holt,I.E.,
            Loftus,B.J., Ujwal,M.L., Yang,F., Smith,H.O., Venter,J.C.,
            Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-2001) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
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ORIGIN

  Query Match             41.4%;  Score 990;  DB 1;  Length 11931;
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Qy    478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
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Qy    838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897
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Qy   1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545
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Qy   2146 TGAGCCAGAAG 2156
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Db   8118 TGAATCTGATG 8128
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RESULT 13
SPNEU1901
LOCUS       SPNEU1901             232807 bp    DNA     linear   HTG 12-JUL-2001
DEFINITION  Streptococcus pneumoniae clone G54, *** SEQUENCING IN PROGRESS ***,
            in ordered pieces.
ACCESSION   AL449923
VERSION     AL449923.1  GI:11545148
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Streptococcus pneumoniae.
  ORGANISM  Streptococcus pneumoniae
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 232807)
  AUTHORS   Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Humbert,Y.,
            Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de
            Francesco,M., Polissi,A., Buell,G., Feger,G., Garcia,E., Peitsch,M.
            and Garcia-Bustos,J.F.
  TITLE     Annotated draft genomic sequence from a Streptococcus pneumoniae
            type 19F clinical isolate
  JOURNAL   Microb. Drug Resist. 7 (2), 99-125 (2001)
  MEDLINE   21335329
   PUBMED   11442348
REFERENCE   2  (bases 1 to 232807)
  AUTHORS   Dopazo,J., Mendoza,A., Herrero,J., Caldara,F., Polissi,A.,
            Humbert,Y., Friedli,L., Guerrier,M., Grand-Schenk,E., Gandin,C., de
            Francesco,M., Buell,G., Feger,G., Garcia,E., Peitsch,M. and
            Garcia-Bustos,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-OCT-2000) Research Department, Glaxo Wellcome, S.A.,
            Severo Ochoa 2, 28760 Tres Cantos, SPAIN
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COMMENT     * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
FEATURES             Location/Qualifiers
     source          1. .232807
                     /organism="Streptococcus pneumoniae"
                     /serotype="19F"
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ORIGIN
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  Matches 1616;  Conservative    0;  Mismatches  697;  Indels  150;  Gaps    6;

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Qy      58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117
           ||||||||||  | || ||     |||||  | || |||||||| || ||||| || ||
Db  200412 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAATTTGACACCAGATGAAGTCAG 200471

Qy     118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
           ||| | || || ||||| || || ||||| || |||||||| || || ||||| |||||
Db  200472 TAAGAGGGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT 200531

Qy     178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237
           || || ||||| ||||| |||||||| || ||||| |||||||||||||| || |||||
Db  200532 GACCTCTATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT 200591

Qy     238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297
           |||||||||  | |||||||||||||| || ||| || | || |||   || ||||| ||
Db  200592 CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA 200651

Qy     298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
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Qy     358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCA 417
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Db  200712 TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACG 200771

Qy     418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477
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Qy     478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
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Db  200823 CCAAGGACGCTACACCACAGATGATGGTTATATCTTTAATGCTTCTGATATCATTGAAGA 200882

Qy     538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
           |||||||||||| ||||||||||||||||  |||| | ||| || |||||||||| |||
Db  200883 TACTGGTGATGCCTATATCGTTCCTCATGGCAATCACTTCCACTATATTCCTAAGAGTGA 200942

Qy     598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657
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Qy     658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717
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Db  200988 -GAAGCAGGGATCTCGTCCTTCTTCAAGTTCTAGTCATAATGCAAATCCAGCTCAACCAA 201046

Qy     718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG 777
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Db  201047 GATTGTCAGAGAACCACAATCT-------------------GACTGTCACTCCAACTTA 201086

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Db  201087 TCATCAAAATCAAGGGGAAAACATTTCAAGCCTTTTACGTGAATTGTATGCTAAACCCTT 201146
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Qy     898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957
Db  201207 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACA 201266

Qy     958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017
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Qy    1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
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Qy    1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAA-----------ATTCTTCTTT 1125
Db  201387 AAGTCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATT 201446

Qy    1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
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Qy    1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365
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Qy    1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
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Qy    1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785
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Qy    1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845
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Qy    1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG 1965
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Qy    2126 ----------CCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGA 2175
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RESULT 14
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VERSION	AR120270.1 GI:14103846		
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SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 2290)		
AUTHORS	Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B., Fannon,M.R. and Rosen,C.A.		
TITLE	Streptococcus pneumoniae antigens and vaccines		
JOURNAL	Patent: US 6159469-A 65 12-DEC-2000;		
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source	1. .2290		
	/organism="unknown"		
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ORIGIN			

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Best Local Similarity 67.7%; Pred. No. 1e-200;
Matches 1481; Conservative 0; Mismatches 645; Indels 60; Gaps 5;

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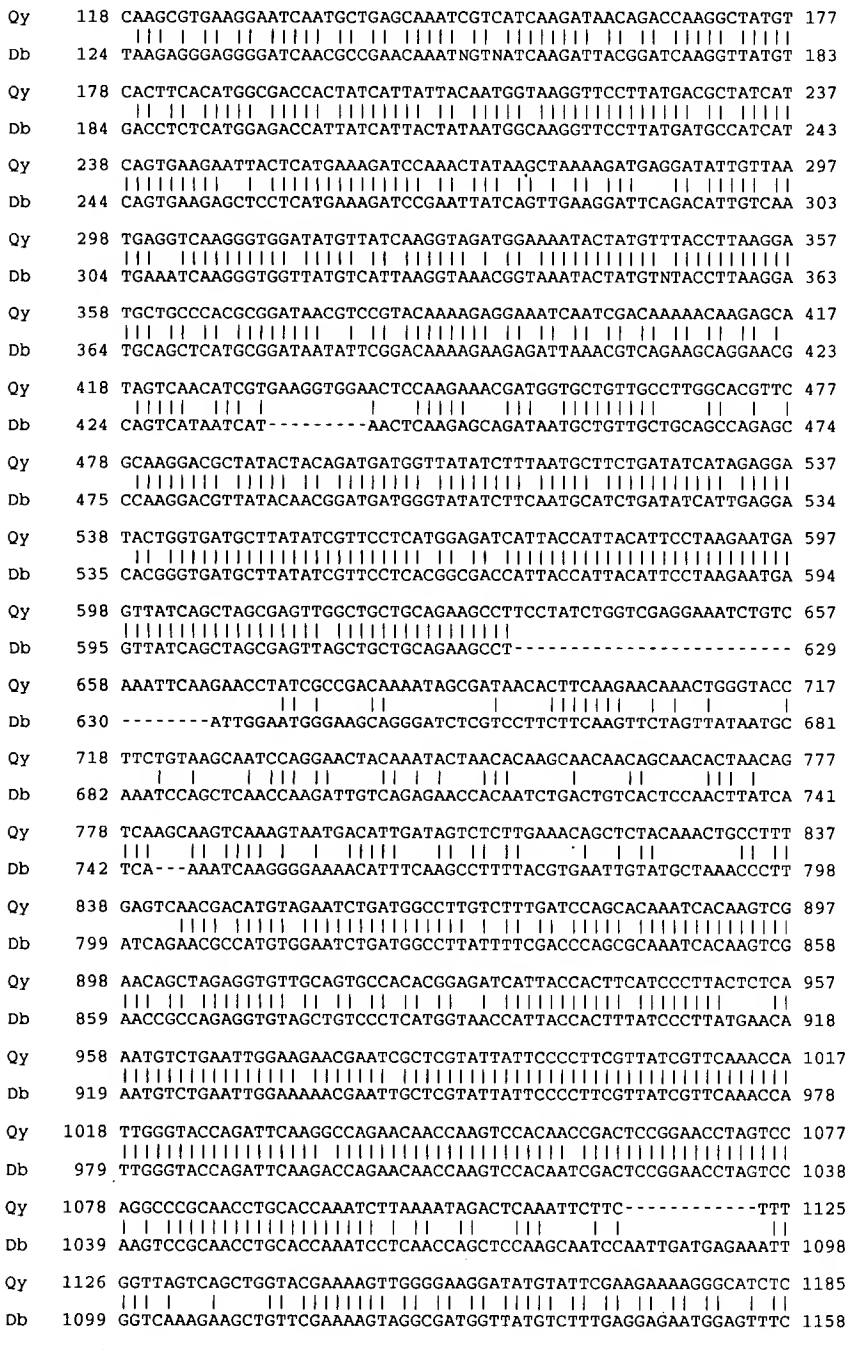

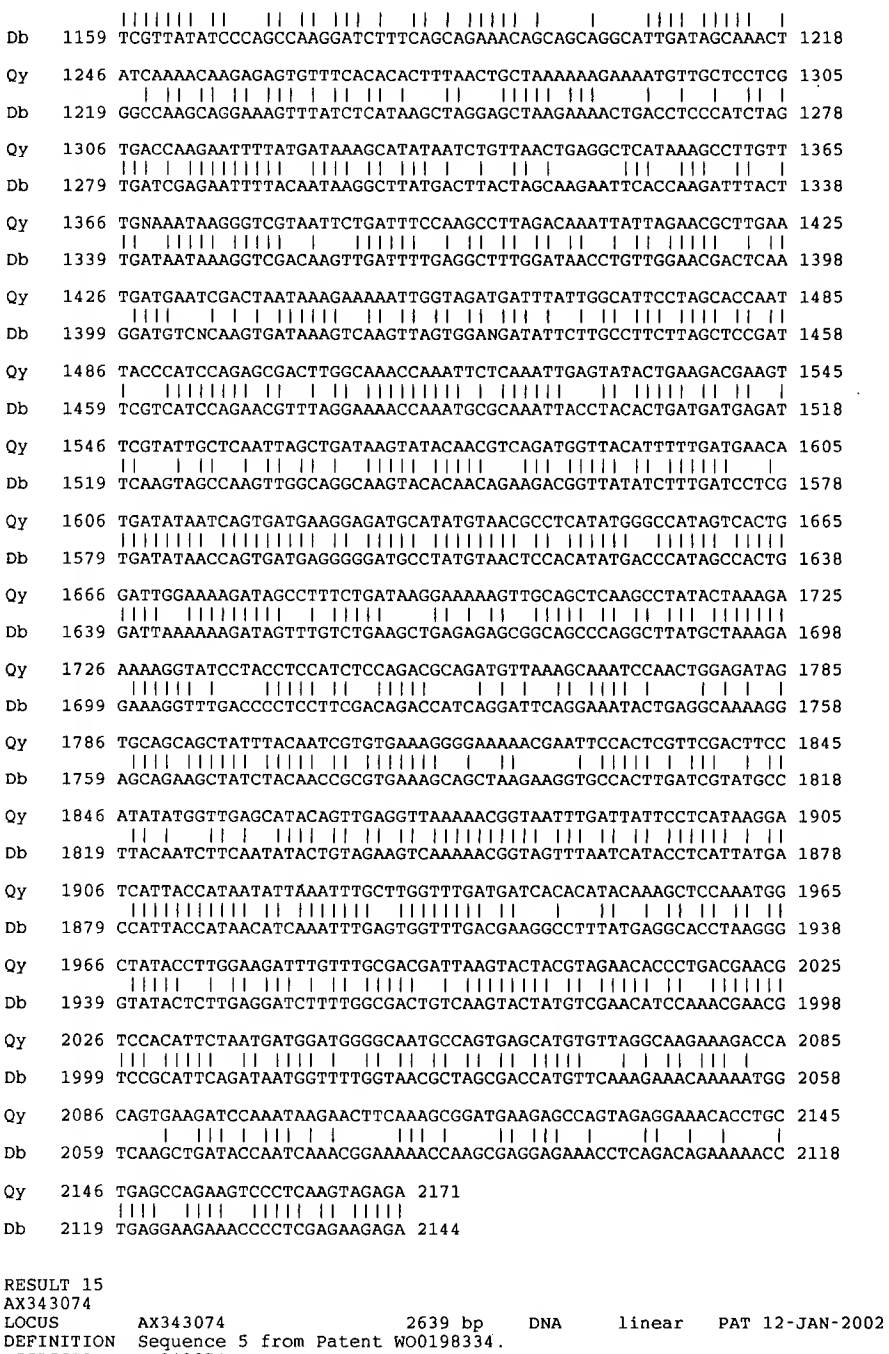

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DEFINITION Sequence 5 from Patent WO0198334.
ACCESSION AX343074

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REFERENCE   1
  AUTHORS   Hamel,J., Ouellet,C., Charland,N., Martin,D. and Brodeur,B.
  TITLE     Streptococcus antigens
  JOURNAL   Patent: WO 0198334-A 5 27-DEC-2001;
            SHIRE BIOCHEM INC. (CA)
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Qy     118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
Db     293 TAAGAGAGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT 352

Qy     178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237
Db     353 GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT 412

Qy     238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297
Db     413 CAGTGAAGAACTTCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA 472

Qy     298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
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Qy     358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCA 417
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Qy     418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477
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Qy     478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
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Qy     538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
Db     704 CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA 763

Qy     598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657
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Qy     778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837
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Qy     898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957
Db    1028 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACA 1087

Qy     958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017
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Qy    1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
Db    1148 TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC 1207

Qy    1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTC------------TTT 1125
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Qy    1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
Db    1268 GGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTC 1327

Qy    1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245
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Qy    1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305
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Qy    1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365
Db    1448 TGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACT 1507

Qy    1366 TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 1425
Db    1508 TGATAATAAAGGTCGACAAGTTGATTTTGAGGTTTTGGATAACCTGTTGGAACGACTCAA 1567

Qy    1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
Db    1568 GGATGTCTCAAGTGATAAAGTCAAGTTAGTGGATGATATTCTTGCCTTCTTAGCTCCGAT 1627

Qy    1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545
Db    1628 TCGTCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGAT 1687

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Qy    1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845
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Qy   1846 ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA 1905
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Db   1988 TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA 2047

Qy   1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG 1965
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Db   2108 GTATAGTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG 2167

Qy   2026 TCCACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCA 2085
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Qy   2146 TGAGCCAGAAG 2156
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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2388	100.0	2389	19	AAV27351	Streptococcus pneu
	2	2388	100.0	2389	24	ABQ84819	S. pneumoniae SP03
	3	2388	100.0	2451	21	AAA47604	Recombinant varian
	4	2388	100.0	8195	19	AAV52227	Streptococcus pneu
	5	1374.2	57.5	2523	21	AAA65731	Streptococcus pneu
	6	1374.2	57.5	2647	21	AAA65736	Streptococcus pneu
	7	1374.2	57.5	2647	24	ABK15103	DNA encoding Strep
	8	1011.8	42.4	2478	21	AAA08557	S. pneumoniae 92 k
	9	1003.8	42.0	2481	21	AAA05417	Streptococcus pneu
	10	991	41.5	2531	21	AAA47605	Recombinant varian
	11	990	41.4	2531	21	AAA47602	Recombinant varian
	12	987.6	41.3	2290	19	AAV27356	Streptococcus pneu
	13	987.6	41.3	2290	24	ABQ84824	S. pneumoniae SP04
	14	980.8	41.1	2639	21	AAA65737	Streptococcus pneu
	15	980.8	41.1	2639	24	ABK15104	DNA encoding Strep
	16	869.4	36.4	2163	20	AAX25394	Streptococcus pneu
	17	653.8	27.4	2359	19	AAV52376	Streptococcus pneu
	18	548.4	23.0	3171	21	AAA65739	Streptococcus pneu
	19	385.4	16.1	1342	19	AAV27414	Streptococcus pneu
	20	385.4	16.1	1342	24	ABQ84882	S. pneumoniae SP10
	21	385.4	16.1	1455	21	AAA65733	Streptococcus pneu
	22	385.4	16.1	1455	21	AAA47603	Recombinant varian
	23	385.4	16.1	1455	21	AAA05473	Streptococcus pneu
	24	385.4	16.1	1455	21	AAZ91804	Streptococcus pneu
	25	385.4	16.1	3120	21	AAA65730	Streptococcus pneu
	26	385.4	16.1	5048	21	AAA65735	Streptococcus pneu
	27	385.4	16.1	5048	24	ABK15101	DNA encoding Strep
c	28	385.4	16.1	6867	19	AAV52325	Streptococcus pneu
	29	381.4	16.0	973	19	AAV52488	Streptococcus pneu
	30	347	14.5	2528	21	AAA65738	Streptococcus pneu
	31	347	14.5	2528	24	ABK15105	DNA encoding Strep
	32	247.4	10.4	504	21	AAA08556	S. pneumoniae 20 k
	33	243.4	10.2	1684	19	AAV52391	Streptococcus pneu
	34	214.6	9.0	2475	24	ABN66838	Streptococcus poly
	35	214.6	9.0	2478	22	AAS00036	Streptococcus pyog
	36	211.4	8.8	1146	21	AAA05814	Group B Streptococ
	37	211.4	8.8	2466	24	ABN69535	Streptococcus poly
	38	211.4	8.8	2466	24	ABN70334	Streptococcus poly
	39	211.4	8.8	2469	21	AAA05811	Group B Streptococ
	40	211.4	8.8	2469	22	AAS00038	Streptococcus agal
	41	209.8	8.8	2469	21	AAA65740	Streptococcus pneu
	42	209.8	8.8	5215	20	AAX91105	Group B Streptococ
	43	206.6	8.6	2472	21	AAA65741	Streptococcus pneu
	44	201.6	8.4	1398	24	ABN66839	Streptococcus poly
	45	201.2	8.4	819	24	ABK15106	DNA encoding Strep

ALIGNMENTS

RESULT 1
AAV27351
ID AAV27351 standard; DNA; 2389 BP.
XX
AC AAV27351;
XX
DT 02-OCT-1998 (first entry)
XX
DE Streptococcus pneumoniae SP0036 nucleotide.
XX
KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
KW detection; pneumonia; otitis media; meningitis; ss.
XX
OS Streptococcus pneumoniae.
XX
FH Key Location/Qualifiers
FT CDS 2..2389
FT /*tag= a
FT /product= "SP0036"
FT /transl_except= (pos:1367..1369,aa:Xaa)
FT /note= "no stop codon given; Xaa is unspecified"
XX
PN WO9818930-A2.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US19422.
XX
PR 31-OCT-1996; 96US-0029960.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
XX
DR WPI; 1998-272224/24.
DR P-PSDB; AAW55090.
XX
PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
PT pneumoniae - or their epitope-containing fragments, useful in
PT protective or therapeutic vaccines, and for diagnosis
XX
PS Claim 1; Page 59; 118pp; English.
XX
CC The present sequence encodes a protein from Streptococcus pneumoniae.
CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
CC can be useful in vaccines for inducing protective antibodies against
CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
CC are used to detect Streptococcus infection (by usual hybridisation or
CC amplification methods), also for isolating Streptococcus genes or their
CC allelic variants. The protein can be used similarly to detect specific
CC antibodies in standard immunoassays, especially for diagnosing or
CC monitoring infections. Antibodies which bind the protein are used to
CC detect corresponding antigens, to purify the protein and for passive
CC immunisation (optionally coupled to a toxin). Vaccines are administered,
CC e.g. by injection, orally or through the skin, typically at 0.01-1000
CC (especially 10-300) mu g/ml per dose.
XX
SQ Sequence 2389 BP; 830 A; 461 C; 486 G; 611 T; 1 other;

Query Match 100.0%; Score 2388; DB 19; Length 2389;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60

Qy      61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
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Db      61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120

Qy     121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180

Qy     181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240
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Db     181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240

Qy     241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300
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Db     241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300

Qy     301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
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Db     301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360

Qy     361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
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Db     361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420

Qy     421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480

Qy     481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540

Qy     541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600
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Db     541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600

Qy     601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660
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Db     601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660

Qy     661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720
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Db     661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720

Qy     721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780

Qy     781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840

Qy     841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900

Qy     901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960

Qy     961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
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Db     961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020

Qy    1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080

Qy    1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140
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Db    1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140

Qy    1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200

Qy    1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260

Qy    1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
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Db    1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320

Qy    1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380
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Db    1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380

Qy    1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440
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Db    1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440

Qy    1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500

Qy    1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560
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Db    1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560

Qy    1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620
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Qy    1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740
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Db   1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740

Qy   1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800
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Qy   1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860
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Qy   1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920
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Qy   1921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980
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Qy   1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040
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Db   1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040

Qy   2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 2100
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Qy   2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160
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Db   2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160

Qy   2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 2220
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Db   2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 2220

Qy   2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280
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Db   2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280

Qy   2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340

Qy   2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389
```

RESULT 2
ABQ84819
ID ABQ84819 standard; DNA; 2389 BP.
XX
AC ABQ84819;
XX
DT 04-SEP-2002 (first entry)
XX
DE S. pneumoniae SP036 nucleotide sequence SEQ ID NO:55.
XX
KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
KW antibacterial; Streptococcal infection; detection; gene; ds.
XX
OS Streptococcus pneumoniae.
XX
PN US2002061545-A1.
XX
PD 23-MAY-2002.
XX
PF 22-JAN-2001; 2001US-0765272.
XX
PR 30-OCT-1997; 97US-0961083.
XX
PA (CHOI/) CHOI G H.
PA (KUNS/) KUNSCH C A.
PA (BARA/) BARASH S C.
PA (DILL/) DILLON P J.
PA (DOUG/) DOUGHERTY B.
PA (FANN/) FANNON M R.
PA (ROSE/) ROSEN C A.
XX
PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
PI Rosen CA;
XX
DR WPI; 2002-479261/51.
DR P-PSDB; ABP54584.
XX
PT New Streptococcus pneumoniae antigens, useful for detecting
PT Streptococcus and for preventing or attenuating disease caused by
PT Streptococcus infection -
XX
PS Claim 1; Page 27; 70pp; English.
XX
CC ABQ84792 to ABQ84904 represents nucleic acids which encode the
CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669.
CC The S. pneumoniae antigens have antibacterial activity and can be
CC used in vaccines. The S. pneumoniae antigens can also be used to
CC prevent or attenuate a Streptococcal infection in an animal. The
CC polynucleotides encoding the S. pneumoniae antigens can be used to
CC detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent
CC primers used in the cloning of S. pneumoniae ORFs (open reading frames)
CC which are used in an example from the present invention.
XX
SQ Sequence 2389 BP; 830 A; 461 C; 486 G; 611 T; 1 other;

Query Match 100.0%; Score 2388; DB 24; Length 2389;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60
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Db      1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60

Qy     61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
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Db     61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120

Qy    121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180

Qy    181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240
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Db    181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240

Qy    241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300
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Db    241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300

Qy    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
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Db    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360

Qy    361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420

Qy    421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480

Qy    481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540

Qy    541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600
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Qy    601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660

Qy    661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720

Qy    721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780

Qy    781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840

Qy    841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900

Qy    901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960

Qy    961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020

Qy   1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080

Qy   1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140

Qy   1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200

Qy   1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260

Qy   1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320

Qy   1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380

Qy   1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440

Qy   1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500

Qy   1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560

Qy   1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620

Qy   1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1680

Qy   1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740

Qy   1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800

Qy   1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860

Qy   1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920

Qy   1921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980

Qy   1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040

Qy   2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 2100

Qy   2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160

Qy   2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 2220

Qy   2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280

Qy   2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340

Qy   2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389
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RESULT 3
AAA47604
ID AAA47604 standard; DNA; 2451 BP.
XX
AC AAA47604;
XX
DT 20-OCT-2000 (first entry)
XX
DE Recombinant variant of Sp36 gene (Sp36A) of S. pneumoniae.
XX
KW Streptococcus pneumoniae; infection; vaccine; coiled coil region;
KW histidine triad residue; Sp36; antibody; otitis media;
KW nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
KW meningitis; lobar pneumonia; ds.
XX
OS Streptococcus pneumoniae.
XX
FH Key Location/Qualifiers
FT CDS 1..2451
FT /*tag= a
FT /product= Sp36A polypeptide
XX
PN WO200037105-A2.
XX
PD 29-JUN-2000.

XX
PF 21-DEC-1999; 99WO-US30390.
XX
PR 21-DEC-1998; 98US-0113048.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Johnson LS, Koenig S, Adamou JE;
XX
DR WPI; 2000-452129/39.
DR P-PSDB; AAB01468.
XX
PT Vaccine useful for prophylaxis and treatment of pnemococcal infections
PT such as otitis media, nasopharyngeal and bronchial infections,
PT comprises Streptococcus pneumoniae proteins
XX
PS Disclosure; Page 64-65; 70pp; English.
XX
CC Although a number of proteins have been suggested as being involved
CC in the pathogenicity of Streptococcus pneumoniae, there still remains
CC a need to identify polypeptides having epitopes in common from
CC various strains of S. pneumoniae in order to utilise such
CC polypeptides in vaccines to protect against a wide variety of
CC S. pneumoniae. New vaccine compositions are described which comprise a
CC Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
CC acids in length that comprise at least one histidine triad residue
CC (HxxHxH) or a coiled-coil region, or an antibody directed against
CC these features. The vaccine is useful in protecting against infection
CC by Streptococcus pneumoniae. The vaccine composition comprising
CC antibodies to is useful for passive immunization for treating
CC Pneumococcal infections which includes otitis media, nasopharyngeal
CC and bronchial infections.
XX
SQ Sequence 2451 BP; 849 A; 467 C; 499 G; 635 T; 1 other;

Query Match 100.0%; Score 2388; DB 21; Length 2451;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 119

Qy      61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 179

Qy     121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 239

Qy     181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 299

Qy     241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 359

Qy     301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 419

Qy     361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 479

Qy     421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 539

Qy     481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 599

Qy     541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 659

Qy     601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 719

Qy     661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 779

Qy     721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 839

Qy     781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 899

Qy     841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 959

Qy     901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     960 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 1019

Qy     961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1020 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1079

Qy    1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1080 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1139

Qy    1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1199

Qy    1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1259

Qy    1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1260 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1319

Qy    1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1320 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1379

Qy    1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1380 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1439

Qy    1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1440 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1499

Qy    1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1500 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1559

Qy    1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1560 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1619

Qy    1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1620 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1679
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Qy   1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1680 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1739

Qy   1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1740 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1799

Qy   1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1800 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1859

Qy   1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1860 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1919

Qy   1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1920 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1979

Qy   1921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1980 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 2039

Qy   1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2040 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2099

Qy   2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2100 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 2159

Qy   2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2160 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2219

Qy   2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2220 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 2279

Qy   2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2280 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2339

Qy   2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2340 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2399

Qy   2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2400 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2448
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RESULT 4
AAV52227
ID AAV52227 standard; DNA; 8195 BP.
XX
AC AAV52227;
XX
DT 23-OCT-1998 (first entry)
XX
DE Streptococcus pneumoniae genome fragment SEQ ID NO:94.
XX
KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
KW computer readable medium; vaccine; pharmaceutical composition; ds.
XX
OS Streptococcus pneumoniae.
XX
PN WO9818931-A2.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US19588.
XX
PR 31-OCT-1996; 96US-0029960.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M;
PI Kunsch CA, Rosen CA;
XX
DR WPI; 1998-272225/24.
XX
PT Computer-readable medium with recorded Streptococcus pneumoniae
PT polynucleotide sequences - useful in diagnostic kits and assays, and
PT pharmaceutical compositions and vaccines for Streptococcus
PT pneumoniae
XX
PS Claim 1; Page 727-732; 1409pp; English.
XX
CC The present invention describes a computer readable medium which has
CC the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)
CC recorded on it, or a representative fragment or a sequence at least 95%
CC identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in
CC SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from
CC Streptococcus pneumoniae. The present invention also describes an
CC isolated nucleic acid molecule encoding a homologue of any of the
CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the
CC nucleic acid molecule is produced by a process comprising: (a) screening
CC a genomic DNA library using as a probe a target sequence defined by any
CC of the sequences in SEQ ID NO:1 to 391, identifying members of the
CC library which contain sequences that hybridise to the target sequence and
CC isolating the nucleic acid molecules from the members; or (b) isolating
CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid
CC molecules whose nucleotide sequence is homologous to amplification
CC primers derived from the fragment of the S. pneumoniae genome to prime
CC the amplification and isolating the amplified sequences. The computer
CC readable medium can be used in a computer-based system for identifying
CC fragments of the S. pneumoniae genome of commercial importance, or
CC expression modulating fragments of the S. pneumoniae genome. Products
CC from the present invention can be used in diagnosis kits and assays, and
CC pharmaceutical compositions and vaccines for S. pneumoniae.
XX
SQ Sequence 8195 BP; 2688 A; 1622 C; 1777 G; 2105 T; 3 other;

Query Match 100.0%; Score 2388; DB 19; Length 8195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3053 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 3112

Qy     61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3113 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 3172

Qy    121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3173 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 3232

Qy    181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3233 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 3292

Qy    241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3293 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 3352

Qy    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3353 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 3412

Qy    361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3413 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 3472

Qy    421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3473 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 3532

Qy    481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3533 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 3592

Qy    541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3593 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 3652

Qy    601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3653 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 3712

Qy    661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3713 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 3772

Qy    721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3773 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 3832

Qy    781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3833 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 3892

Qy    841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3893 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 3952

Qy    901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3953 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 4012

Qy    961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4013 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 4072

Qy   1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4073 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 4132

Qy   1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4133 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 4192

Qy   1141 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4193 ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTATGTCTTTGC 4252

Qy   1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4253 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 4312

Qy   1261 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4313 TGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 4372

Qy   1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   4373 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGAAAATAAGGGTCG 4432

Qy   1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4433 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 4492

Qy   1441 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4493 TAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 4552

Qy   1501 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4553 ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 4612

Qy   1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4613 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 4672

Qy   1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4673 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 4732

Qy   1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4733 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 4792

Qy   1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4793 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 4852

Qy   1801 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4853 CAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 4912

Qy   1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4913 TACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT 4972

Qy   1921 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4973 TAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 5032

Qy   1981 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5033 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 5092

Qy   2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5093 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAGTGAAGATCCAAA 5152

Qy   2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5153 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 5212

Qy   2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5213 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAA 5272

Qy   2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5273 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 5332

Qy   2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5333 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 5392

Qy   2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 2389
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   5393 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC 5441
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RESULT 5
AAA65731
ID   AAA65731 standard; DNA; 2523 BP.
XX
AC   AAA65731;
XX
DT   21-NOV-2000  (first entry)
XX
DE   Streptococcus pneumoniae BVH-11 gene SEQ ID NO:3.
XX
KW   Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
```

KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal; ds.
XX
OS Streptococcus pneumoniae.
XX
PN WO200039299-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-CA01218.
XX
PR 23-DEC-1998; 98US-0113800.
XX
PA (BIOC-) BIOCHEM PHARMA INC.
XX
PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX
DR WPI; 2000-452397/39.
DR P-PSDB; AAB12716.
XX
PT Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT otitis media, bacteremia and/or pneumonia -
XX
PS Example 2; Fig 3; 106pp; English.
XX
CC The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the protein
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence encodes the
CC S. pneumoniae BVH-11 protein antigen.
XX
SQ Sequence 2523 BP; 879 A; 523 C; 526 G; 595 T; 0 other;

Query Match 57.5%; Score 1374.2; DB 21; Length 2523;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 1819; Conservative 0; Mismatches 539; Indels 102; Gaps 2;

```
Db   1620 AGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCGTGA 1679

Qy   1609 TATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGAT 1668
Db   1680 TATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTGGAT 1739

Qy   1669 TGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAA 1728
Db   1740 TAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGAGAA 1799

Qy   1729 AGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGC 1788
Db   1800 AGGTTTGACCCCTCCTTCGACAGACCATCAGGATTCAGGAAATACTGAGGCAAAAGGAGC 1859

Qy   1789 AGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATA 1848
Db   1860 AGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCCTTA 1919

Qy   1849 TATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCA 1908
Db   1920 CAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGACCA 1979

Qy   1909 TTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTA 1968
Db   1980 TTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGGGTA 2039

Qy   1969 TACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCC 2028
Db   2040 TACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACGTCC 2099

Qy   2029 ACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAG 2088
Db   2100 GCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTCA 2159

Qy   2089 TGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAG---------------------- 2125
Db   2160 AGCTGATACCAATCAAACGGAAAAACCAAGCGAGGAGAAACCTCAGACAGAAAAACCTGA 2219

Qy   2126 ------------------------------------------------------------ 2125
Db   2220 GGAAGAAACCCCTCGAGAAGAGAAACCACAAAGCGAGAAACCAGAGTCTCCAAAACCAAC 2279

Qy   2126 -------CCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA 2178
Db   2280 AGAGGAACCAGAAGAAGAATCACCAGAGGAATCAGAAGAACCTCAGGTCGAGACTGAAAA 2339

Qy   2179 AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT 2238
Db   2340 GGTTGAAGAAAAACTGAGAGAGGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTAT 2399

Qy   2239 GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT 2298
Db   2400 CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA 2459

Qy   2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358
Db   2460 GGACAACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA 2519
```

RESULT 6
AAA65736
ID AAA65736 standard; DNA; 2647 BP.
XX
AC AAA65736;
XX
DT 21-NOV-2000 (first entry)
XX
DE Streptococcus pneumoniae BVH-11 gene SEQ ID NO:12.
XX
KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal; ds.
XX
OS Streptococcus pneumoniae.
XX
PN WO200039299-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-CA01218.
XX
PR 23-DEC-1998; 98US-0113800.
XX
PA (BIOC-) BIOCHEM PHARMA INC.
XX
PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX
DR WPI; 2000-452397/39.
XX
PT Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT otitis media, bacteremia and/or pneumonia -
XX
PS Example 6; Fig 15; 106pp; English.
XX
CC The present invention describes nucleic acids (I) encoding protein
CC antigens (II) from Streptococcus pneumoniae. The protein antigens
CC have bactericidal activity. The nucleic acids, encoding the protein
CC antigens, may be used for the recombinant production of the proteins
CC they encode. The protein antigens may then be used as vaccines for the
CC prevention and treatment of Streptococcal infections in mammals
CC (especially humans) which result in, e.g. meningitis, otitis media,
CC bacteraemia and/or pneumonia. The present sequence encodes the
CC S. pneumoniae BVH-11 protein antigen.
XX
SQ Sequence 2647 BP; 934 A; 538 C; 556 G; 619 T; 0 other;

Query Match 57.5%; Score 1374.2; DB 21; Length 2647;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 1819; Conservative 0; Mismatches 539; Indels 102; Gaps 2;

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Qy      1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60
Db    104 TGCTTATGAACTAGGTTTGCATCAAGCTCAAACTGTAAAAGAAAATAATCGTGTTTCCTA 163

Qy     61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
Db    164 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 223

Qy    121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
Db    224 GCGTGAAGGAATCAACGCCGAACAAATCGTCATCAAGATTACGGATCAAGGTTATGTGAC 283

Qy    181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240
Db    284 CTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCATCAG 343

Qy    241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300
Db    344 TGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAATGA 403

Qy    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
Db    404 AATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTTTACCTTAAGGATGC 463

Qy    361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
Db    464 AGCTCATGCGGATAATGTCCGTACAAAAGAAGAAATCAATCGGCAAAAACAAGAACATAG 523

Qy    421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480
Db    524 TCAGCATCGTGAAGGAGGGACTTCAGCAAACGATGGTGCGGTAGCCTTTGCACGTTCACA 583

Qy    481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540
Db    584 GGGACGCTACACCACAGATGATGGTTATATCTTCAATGCATCTGATATCATCGAAGATAC 643
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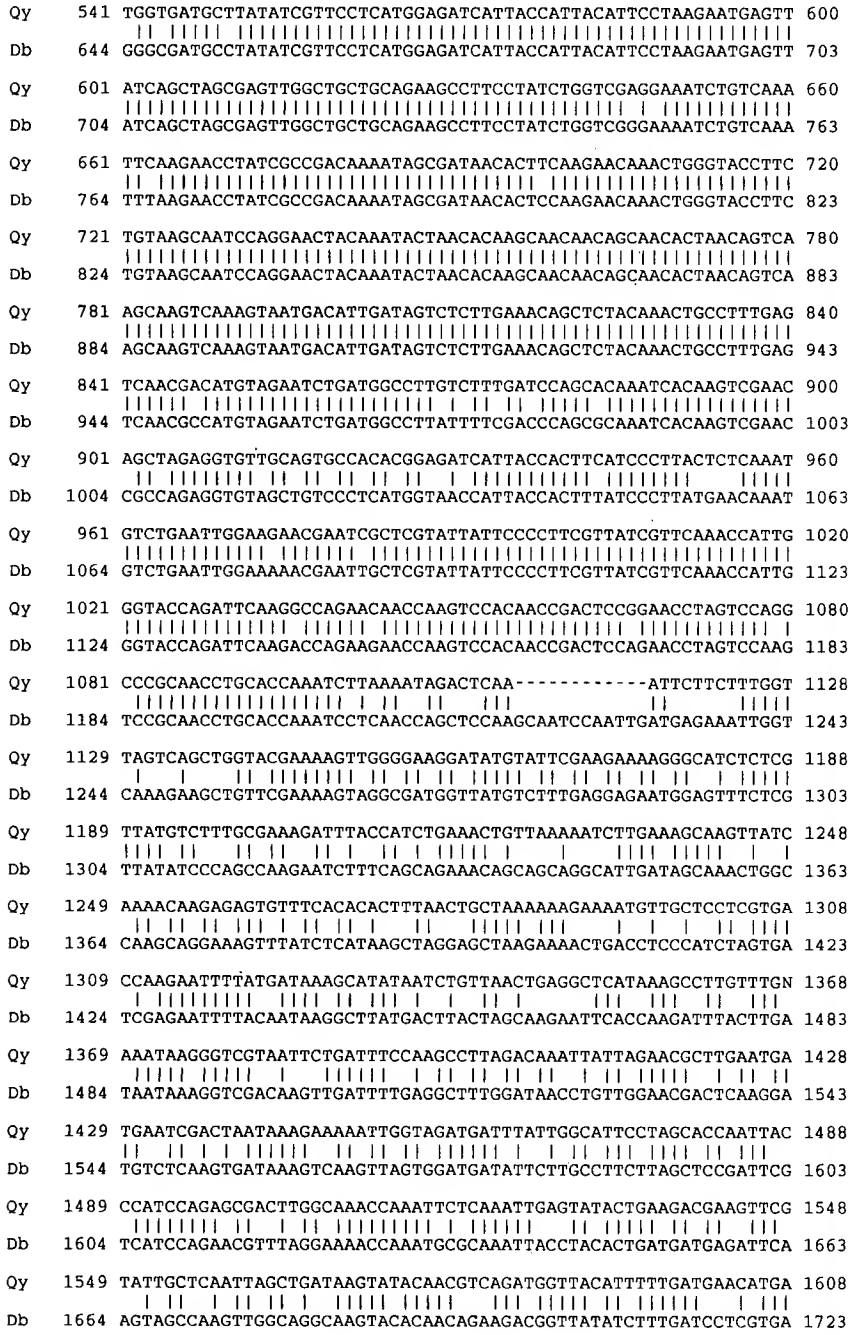

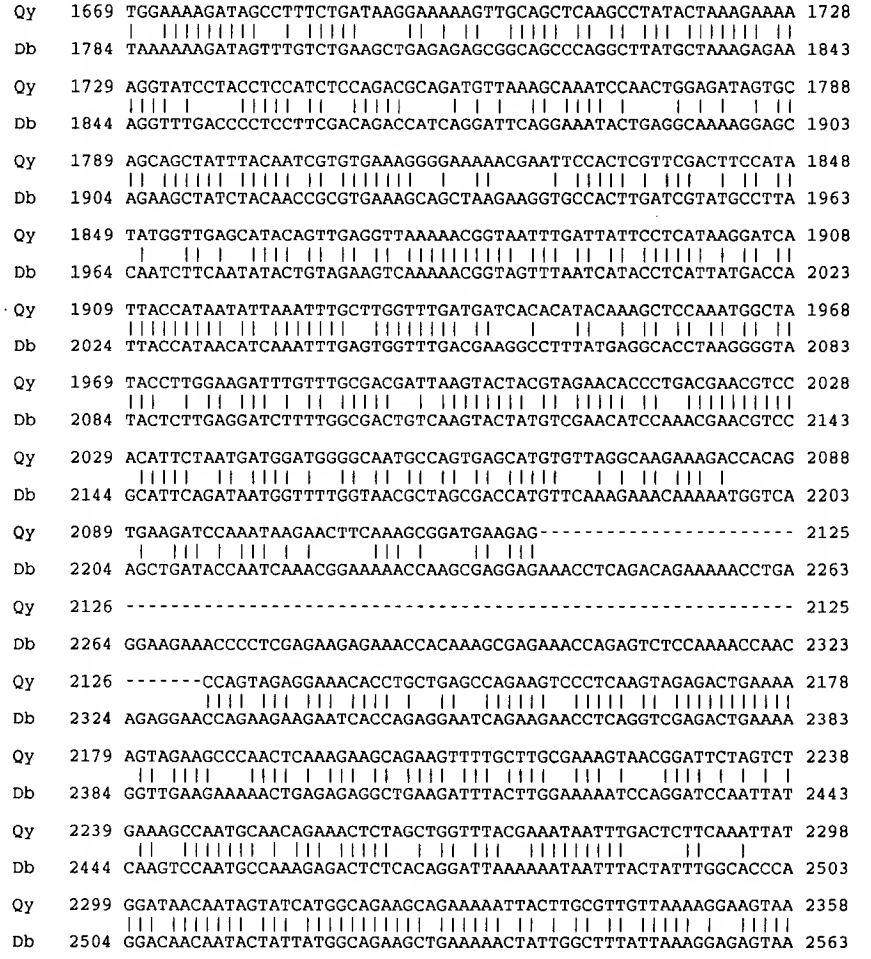

RESULT 7
ABK15103
ID ABK15103 standard; DNA; 2647 BP.
XX
AC ABK15103;
XX
DT 08-MAY-2002 (first entry)
XX
DE DNA encoding Streptococcus pneumoniae BVH-11.
XX
KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW pneumonia; streptococcal bacterial infection; gene; ds.
XX
OS Streptococcus pneumoniae.
XX
FH Key Location/Qualifiers

```
FT   CDS             45..2567
FT                   /*tag=  a
FT                   /product= "BVH-11"
FT                   /note= "The gene is flanked by sequences from the
FT                          vector SP64, no information on which is
FT                          given in the specification"
XX
PN   WO200198334-A2.
XX
PD   27-DEC-2001.
XX
PF   19-JUN-2001; 2001WO-CA00908.
XX
PR   20-JUN-2000; 2000US-212683P.
XX
PA   (SHIR-) SHIRE BIOCHEM INC.
XX
PI   Hamel J,  Ouellet C,  Charland N,  Martin D,  Brodeur B;
XX
DR   WPI; 2002-122272/16.
DR   P-PSDB; AAU75933.
XX
PT   New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT   epitope-bearing polypeptides, useful as vaccine components for treating
PT   or preventing streptococcal infections such as otitis media,
PT   meningitis, and bacteraemia  -
XX
PS   Disclosure; Fig 4; 113pp; English.
XX
CC   The invention describes an isolated polypeptide (I) with 70-90%
CC   identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC   BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC   comprising (I) is useful for therapeutic or prophylactic treatment of
CC   meningitis, otitis media, bacteraemia or pneumonia infection in an
CC   individual susceptible to these disorders. (II) is also useful for
CC   therapeutic or prophylactic treatment of any streptococcal bacterial
CC   infection (e.g., caused by Streptococcus pneumoniae, group A
CC   Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC   as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or
CC   Staphylococcus aureus) in an individual susceptible to the infection.
CC   A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC   techniques. The Streptococcus polypeptides are useful in a diagnostic
CC   test for S. pneumoniae infection. (III) is useful for designing DNA
CC   probes for use in detecting the presence of Streptococcus in a biological
CC   sample suspected of containing the bacteria. The DNA probes may also be
CC   used for detecting circulating S. pneumonia nucleic acid in a sample for
CC   diagnosing streptococcal infections. This sequence encodes the
CC   Streptococcus pneumoniae protein BVH-11, used to create the antigenic
CC   peptides described in the method of the invention.
XX
SQ   Sequence 2647 BP; 934 A; 538 C; 556 G; 619 T; 0 other;

  Query Match             57.5%;  Score 1374.2;  DB 24;  Length 2647;
  Best Local Similarity   73.9%;  Pred. No. 0;
  Matches 1819;  Conservative    0;  Mismatches  539;  Indels  102;  Gaps    2;

Qy      1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60
          | ||||  ||  | ||  || ||||||||  ||| || || ||||||||||||||||||||
Db    104 TGCTTATGAACTAGGTTTGCATCAAGCTCAAACTGTAAAAGAAAATAATCGTGTTTCCTA 163

Qy     61 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    164 TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 223

Qy    121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
          |||||||||||||||| || || |||||||||||||||| || || ||||| ||||| ||
Db    224 GCGTGAAGGAATCAACGCCGAACAAATCGTCATCAAGATTACGGATCAAGGTTATGTGAC 283

Qy    181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG 240
          || ||||| ||||| |||||||| || ||||| ||||| |||||||| || ||||||||
Db    284 CTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCATCAG 343

Qy    241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 300
          ||||||  | ||||||||||||||| || ||| || | || |||   || ||||| ||||||
Db    344 TGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAATGA 403

Qy    301 GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC 360
          ||||||||| ||||| || |||||| | || ||||||||||||||||||||||||||||||
Db    404 AATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTTTACCTTAAGGATGC 463

Qy    361 TGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCATAG 420
          || || |||||||| |||||||||||||| |||||||||| |||||||||| ||||||
Db    464 AGCTCATGCGGATAATGTCCGTACAAAAGAAGAAATCAATCGGCAAAAACAAGAACATAG 523

Qy    421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 480
          ||| |||||||||||| || ||| ||  |||||||||||| || ||||| ||||||||||
Db    524 TCAGCATCGTGAAGGAGGGACTTCAGCAAACGATGGTGCGGTAGCCTTTGCACGTTCACA 583

Qy    481 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 540
          |||||||| || |||||||||||||||||||| ||||| |||||||||| || ||||||
Db    584 GGGACGCTACACCACAGATGATGGTTATATCTTCAATGCATCTGATATCATCGAAGATAC 643

Qy    541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600
          || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    644 GGGCGATGCCTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 703

Qy    601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660
          |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Db    704 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGGGAAAATCTGTCAAA 763

Qy    661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720
          || |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    764 TTTAAGAACCTATCGCCGACAAAATAGCGATAACACTCCAAGAACAAACTGGGTACCTTC 823

Qy    721 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    824 TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAGTCA 883

Qy    781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 943

Qy    841 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC 900
          |||||| |||||||||||||||||||| | || || ||||| ||||||||||||||||||
Db    944 TCAACGCCATGTAGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGTCGAAC 1003

Qy    901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960
          || |||||||| || || || || ||  | |||||||||||| ||||||||    |||||
Db   1004 CGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACAAAT 1063

Qy    961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
          |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||
Db   1064 GTCTGAATTGGAAAAACGAATTGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1123

Qy   1021 GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG 1080
          |||||||||||||||| |||||| |||||||||||||||||||||| ||||||||||| |
Db   1124 GGTACCAGATTCAAGACCAGAAGAACCAAGTCCACAACCGACTCCAGAACCTAGTCCAAG 1183

Qy   1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAA-----------ATTCTTCTTTGGT 1128
          |||||||||||||||||| | ||  ||   |||            ||      |||||
Db   1184 TCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATTGGT 1243

Qy   1129 TAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCG 1188
          |   |    || |||||||| || || || ||||| || || || || ||  | |||||
Db   1244 CAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTCTCG 1303

Qy   1189 TTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATC 1248
          |||| ||   || ||  || |  || | ||||| |     |    |||| ||||| |  |
Db   1304 TTATATCCCAGCCAAGAATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACTGGC 1363

Qy   1249 AAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGA 1308
          || || || ||| | || || |   ||  ||||| |||    |  |  |  || ||||
Db   1364 CAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAGTGA 1423

Qy   1309 CCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGN 1368
          | |||||||||  |||| || ||| |  |  || |      |||  |||  ||  |||
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Db   1424 TCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACTTGA 1483

Qy   1369 AAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGA 1428
          ||||| ||||| |   |||||| | || || || ||  | || |||| | || ||
Db   1484 TAATAAAGGTCGACAAGTTGATTTTGAGGCTTTGGATAACCTGTTGGAACGACTCAAGGA 1543

Qy   1429 TGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTAC 1488
          ||  || | | |||||| || || || |||||| | | || ||| |||| || |||
Db   1544 TGTCTCAAGTGATAAAGTCAAGTTAGTGGATGATATTCTTGCCTTCTTAGCTCCGATTCG 1603

Qy   1489 CCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCG 1548
          |||||||| ||  | || ||||||||| | ||||||  || ||||| || ||  |||
Db   1604 TCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGATTCA 1663

Qy   1549 TATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGA 1608
            | ||  | || || |  ||||| |||||   ||| ||||| || ||||||   | |||
Db   1664 AGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCGTGA 1723

Qy   1609 TATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGAT 1668
          ||||| ||||||||| || ||||| |||||||| || |||||| |||||| ||||||||
Db   1724 TATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTGGAT 1783

Qy   1669 TGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAA 1728
          |  |||||||||  | |||||    || | ||  ||||| || || ||| ||||||| ||
Db   1784 TAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGAGAA 1843

Qy   1729 AGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGC 1788
          |||| |    ||||| ||  |||||    | | |  || |||| |    | | |  | ||
Db   1844 AGGTTTGACCCCTCCTTCGACAGACCATCAGGATTCAGGAAATACTGAGGCAAAAGGAGC 1903

Qy   1789 AGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATA 1848
          || |||||| ||||| || ||||||| | ||    | ||||| | |||  | || ||
Db   1904 AGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCCTTA 1963

Qy   1849 TATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGATCA 1908
          |   || |  ||| || || || |||||||||| ||| || || |||||| | || ||
Db   1964 CAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGACCA 2023

Qy   1909 TTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGGCTA 1968
          ||||||||| || ||||||| |||||||| ||    |   ||  | || || || || ||
Db   2024 TTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGGGTA 2083

Qy   1969 TACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCC 2028
          |||  | || ||| | || |||||  | |||||||| || ||||| ||  ||||||||||
Db   2084 TACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACGTCC 2143

Qy   2029 ACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCACAG 2088
          |||||  || |||| |  || || || || || |||||   | | || ||| |
Db   2144 GCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGGTCA 2203

Qy   2089 TGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAG---------------------- 2125
          |  ||| | ||| | |     ||| |    || |||
Db   2204 AGCTGATACCAATCAAACGGAAAAACCAAGCGAGGAGAAACCTCAGACAGAAAAACCTGA 2263

Qy   2126 ------------------------------------------------------------ 2125

Db   2264 GGAAGAAACCCCTCGAGAAGAGAAACCACAAAGCGAGAAACCAGAGTCTCCAAAACCAAC 2323

Qy   2126 -------CCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA 2178
                |||| ||| ||| |||| |  ||  ||||||  ||||| || ||||||||||
Db   2324 AGAGGAACCAGAAGAAGAATCACCAGAGGAATCAGAAGAACCTCAGGTCGAGACTGAAAA 2383

Qy   2179 AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT 2238
          || ||||   |||| | ||| || |||| ||| ||||  ||| |   |||| | | | |
Db   2384 GGTTGAAGAAAAACTGAGAGAGGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTAT 2443

Qy   2239 GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT 2298
          ||  ||||||| | ||| |||||  | || |||  |||||||||     ||   |
Db   2444 CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA 2503

Qy   2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358
          ||| ||||||| ||| |||||||||||| |||||| || | || || ||||| |  |||||
Db   2504 GGACAACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA 2563
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RESULT 8
AAA08557
ID AAA08557 standard; DNA; 2478 BP.
XX
AC AAA08557;
XX
DT 19-JUL-2000 (first entry)
XX
DE S. pneumoniae 92 kDa human C3-degrading protein coding sequence.
XX
KW Human C3-degrading protein; 92 kDa; immunostimulatory; vaccine;
KW inhibitor; inflammation; organ rejection; xenotransplantation; ss.
XX
OS Streptococcus pneumoniae.
XX
PN WO200017370-A1.
XX
PD 30-MAR-2000.
XX
PF 24-SEP-1999; 99WO-US22362.
XX
PR 24-SEP-1998; 98US-0101736.
PR 31-MAR-1999; 99US-0283094.
XX
PA (MINU) UNIV MINNESOTA.
PA (AMCY) AMERICAN CYANAMID CO.
XX
PI Hostetter MK, Finkel DJ, Cheng Q, Green BA, Masi AW;
XX
DR WPI; 2000-283594/24.
DR P-PSDB; AAY91939.
XX
PT Isolated polypeptide is used to stimulate immune system and immunize or
PT treat a mammalian subject against Streptococcus pneumoniae infection or
PT colonization
XX
PS Claim 1; Page 55-57; 63pp; English.
XX
CC The present sequence, isolated from Streptococcus pneumoniae, encodes a
CC human C3-degrading protein (see AAY91939) of about 92 kDa. This
CC sequence may encompass a smaller 20 kDa polypeptide coding sequence
CC (AAA08556) also having human C3-degrading activity.
CC The DNA sequences can be used for producing an immune response to
CC Streptococcus pneumoniae in a mammal. Antibodies against the proteins
CC can be used to inhibit S. pneumoniae-mediated C3 degradation.
CC C3-mediated inflammation and rejection in xenotransplantation can be
CC inhibited by expressing the nucleic acid sequences on the surface of an
CC organ of an animal. In particular, the polypeptides are useful for
CC stimulating the immune system and are effective to immunize or treat a
CC mammalian subject against Streptococcus pneumoniae infection or
CC colonization.
XX
SQ Sequence 2478 BP; 837 A; 510 C; 535 G; 596 T; 0 other;

Query Match 42.4%; Score 1011.8; DB 21; Length 2478;
Best Local Similarity 66.2%; Pred. No. 3.8e-244;
Matches 1628; Conservative 0; Mismatches 688; Indels 144; Gaps 6;

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Qy      1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC 57
          ||| || ||  | || |   | |||||| |   ||||||| || |   |||||| |||||
Db     60 TTCCTATGAACTTGGTCGTCACCAAGCTGGTCAGGTTAAGAAAGAGTCTAATCGAGTTTC 119

Qy     58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117
            ||||||||||  | || ||    |||||  | || || ||||| || ||||| || ||
Db    120 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG 179

Qy    118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
          ||| | || || ||||| || || ||||||||||||||||| || || ||||| |||||
Db    180 TAAGAGGGAGGGGATCAACGCCGAACAAATCGTCATCAAGATTACGGATCAAGGTTATGT 239

Qy    178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237
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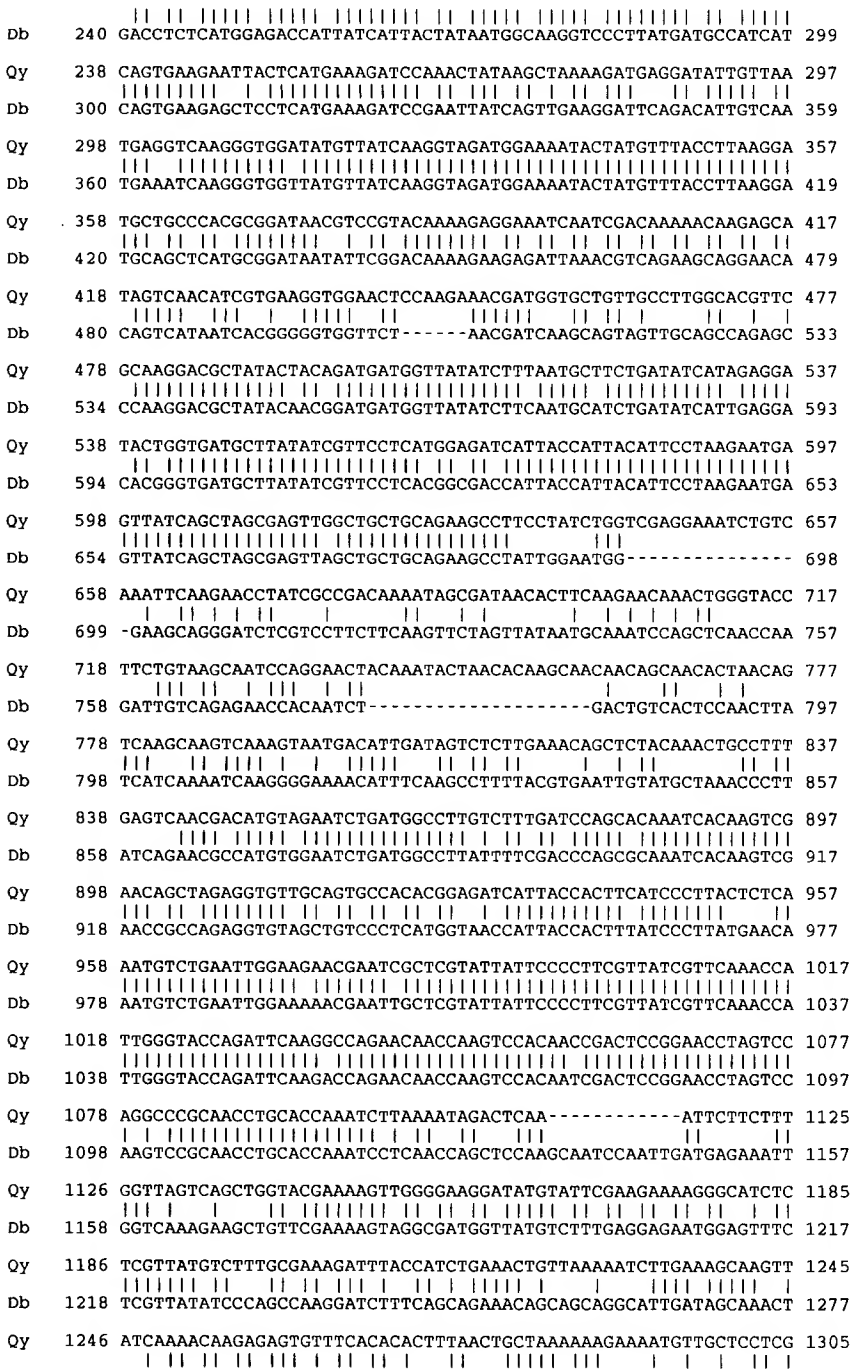
Db 240 GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCAT 299
Qy 238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297
Db 300 CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA 359
Qy 298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
Db 360 TGAAATCAAGGGTGGTTATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 419
Qy 358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCA 417
Db 420 TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACA 479
Qy 418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477
Db 480 CAGTCATAATCACGGGGGTGGTTCT------AACGATCAAGCAGTAGTTGCAGCCAGAGC 533
Qy 478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
Db 534 CCAAGGACGCTATACAACGGATGATGGTTATATCTTCAATGCATCTGATATCATTGAGGA 593
Qy 538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
Db 594 CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA 653
Qy 598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657
Db 654 GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCTATTGGAATGG--------------- 698
Qy 658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717
Db 699 -GAAGCAGGGATCTCGTCCTTCTTCAAGTTCTAGTTATAATGCAAATCCAGCTCAACCAA 757
Qy 718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG 777
Db 758 GATTGTCAGAGAACCACAATCT-------------------GACTGTCACTCCAACTTA 797
Qy 778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837
Db 798 TCATCAAAATCAAGGGGAAAACATTTCAAGCCTTTTACGTGAATTGTATGCTAAACCCTT 857
Qy 838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897
Db 858 ATCAGAACGCCATGTGGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGTCG 917
Qy 898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957
Db 918 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACA 977
Qy 958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017
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Qy 1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
Db 1038 TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC 1097
Qy 1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAA-----------ATTCTTCTTT 1125
Db 1098 AAGTCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATT 1157
Qy 1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
Db 1158 GGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTC 1217
Qy 1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245
Db 1218 TCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT 1277
Qy 1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305
Db 1278 GGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAG 1337
Qy 1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365
Db 1338 TGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACT 1397
Qy 1366 TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 1425
Db 1398 TGATAATAAAGGTCGACAAGTTGATTTTGAGGCTTTGGATAACCTGTTGGAACGACTCAA 1457
Qy 1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
Db 1458 GGATGTCCCAAGTGATAAAGTCAAGTTAGTGGATGATATTCTTGCCTTCTTAGCTCCGAT 1517
Qy 1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545
Db 1518 TCGTCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGAT 1577
Qy 1546 TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA 1605
Db 1578 TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG 1637
Qy 1606 TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG 1665
Db 1638 TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG 1697
Qy 1666 GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA 1725
Db 1698 GATTAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGA 1757
Qy 1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785
Db 1758 GAAAGGTTTGACCCCTCCTTCGACAGACCATCAGGATTCAGGAAATACTGAGGCAAAAGG 1817
Qy 1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845
Db 1818 AGCAGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCC 1877
Qy 1846 ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA 1905
Db 1878 TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA 1937
Qy 1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG 1965
Db 1938 CCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGG 1997
Qy 1966 CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG 2025
Db 1998 GTATACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG 2057
Qy 2026 TCCACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCA 2085
Db 2058 TCCGCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGG 2117
Qy 2086 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGA---------- 2121
Db 2118 TCAAGCTGATACCAATCAAACGGAAAAACCAAGCGAGGAGAAACCTCAGACAGAAAAACC 2177
Qy 2122 ---------- 2121
Db 2178 TGAGGAAGAAACCCCTCGAGAAGAGAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAACC 2237
Qy 2122 ---AGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA 2178
Db 2238 AACAGAGGAACCAGAAGAATCACCAGAGGAATCAGAAGAACCTCAGGTCGAGACTGAAAA 2297
Qy 2179 AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT 2238
Db 2298 GGTTGAAGAAAAACTGAGAGAGGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTAT 2357
Qy 2239 GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT 2298
Db 2358 CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA 2417

```
Qy   2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358
          ||| |||||||| ||| ||||||||||| |||||| || | || || ||||| |  |||||
Db   2418 GGACAACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA 2477


RESULT 9
AAA05417
ID   AAA05417 standard; DNA; 2481 BP.
XX
AC   AAA05417;
XX
DT   24-MAY-2000  (first entry)
XX
DE   Streptococcus pneumoniae nucleotide sequence ID311.
XX
KW   Streptococcus pneumoniae; vaccine; screening; protein antigen;
KW   antibacterial; antiinflammatory; meningitis; infection; diagnosis;
KW   pneumococcal disease; ds.
XX
OS   Streptococcus pneumoniae.
XX
PN   WO200006737-A2.
XX
PD   10-FEB-2000.
XX
PF   27-JUL-1999;   99WO-GB02451.
XX
PR   27-JUL-1998;   98GB-0016337.
PR   19-MAR-1999;   99US-0125164.
XX
PA   (MICR-) MICROBIAL TECHNICS LTD.
XX
PI   Gilbert CFG,  Hansbro PM;
XX
DR   WPI; 2000-195300/17.
DR   P-PSDB; AAY81662.
XX
PT   New Streptococcal protein, useful as a vaccine, for diagnosis of
PT   pneumococcal diseases and for screening agents capable of antagonizing
PT   or inhibiting expression of the protein  -
XX
PS   Claim 2; Page 99; 108pp; English.
XX
CC   AAY81501 to AAY81679 represent specifically claimed protein sequences
CC   isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent
CC   specifically claimed nucleotide sequences isolated from S. pneumoniae.
CC   The sequences have antibacterial and antiinflammatory properties.
CC   The protein sequences, and fragments of them, are useful as immunogens
CC   and/or antigens. The nucleotide sequences can be used in vaccines and in
CC   diagnostic assays. The proteins and nucleotides can be useful for the
CC   detection and diagnosis of S. pneumoniae. The protein sequences are also
CC   useful for screening an agent capable of antagonising, inhibiting or
CC   interfering with the function or expression of the proteins in which the
CC   agent is useful for treatment or prophylaxis of S. pneumoniae infection
CC   and meningitis. AAA05591 to AAA05614 represent primers used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 2481 BP; 839 A; 514 C; 538 G; 590 T; 0 other;

  Query Match             42.0%;  Score 1003.8;  DB 21;  Length 2481;
  Best Local Similarity   66.0%;  Pred. No. 3.9e-242;
  Matches 1623;  Conservative    0;  Mismatches  693;  Indels  144;  Gaps    6;

Qy       1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC 57
             ||| || ||| | || |   | |||||| |   || |||| || |   |||||| ||| |
Db      60 TTCCTATGAGCTTGGTCGTCACCAAGCTGGTCAGGATAAGAAAGAGTCTAATCGAGTTGC 119

Qy      58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117
           ||||||||||||  | || ||    |||||  | || || ||||| || ||||| || ||
Db     120 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG 179

Qy     118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
                ||| | || || ||||| || || |||||||||||||||||| || || ||||| |||||
Db     180 TAAGAGGGAGGGGATCAACGCCGAACAAATCGTCATCAAGATTACGGATCAAGGTTATGT 239

Qy     178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237
           || || ||||| ||||| |||||||| || ||||| ||||| |||||||| || |||||
Db     240 GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCAT 299

Qy     238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297
           |||||||||  | ||||||||||||||| || ||| || | || |||   || ||||| ||
Db     300 CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA 359

Qy     298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
           |||  |||||||||| ||||| |||||||||| ||||||||||||||||||||||||||
Db     360 TGAAATCAAGGGTGGTTATGTCATCAAGGTAGACGGAAAATACTATGTTTACCTTAAGGA 419

Qy     358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCA 417
           ||| || || |||||||  | || |||||||| || || || || || || || || | |
Db     420 TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACG 479

Qy     418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477
           |||||  |||  |     ||| ||      ||||||  ||| || ||    ||  |  |
Db     480 CAGTCATAATCACGGGTCAGGAGCT------AACGATCATGCAGTAGCTGCAGCCAGAGC 533

Qy     478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
           |||||||||||||| || |||||||| |||||||| ||||| |||||||||| |||||
Db     534 CCAAGGACGCTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA 593

Qy     538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
           || ||||||||||||||||||||||| || || ||||||||||||||||||||||||||
Db     594 CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA 653

Qy     598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657
           ||||||||||||||||| ||||||||||||||        |||
Db     654 GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCTATTGGAATGG--------------- 698

Qy     658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717
             |  || | | ||    |      ||   | |       |  | | | | ||
Db     699 -GAAGCAGGGATCTCGTCCTTCTTCAAGTTCTAGTTATAATGCAAATCCAGCTCAACCAA 757

Qy     718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG 777
              ||| ||  | |||  | ||                      |    ||   | |
Db     758 GATTGTCAGAGAACCACAATCT-------------------GACTGTCACTCCAACTTA 797

Qy     778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837
           |||   || |||| |  |  |||||   || || ||      |  | ||       || ||
Db     798 TCATCAAAATCAAGGGGAAAACATTTCAAGCCTTTTACGTGAATTGTATGCTAAACCCTT 857

Qy     838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897
               |||| ||||| |||||||||||||| | || || ||||| ||||||||||||||
Db     858 ATCAGAACGCCATGTGGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGTCG 917

Qy     898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957
           ||| || |||||||| || || || || ||  | |||||||||| ||||||||    ||
Db     918 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACA 977

Qy     958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017
           |||||||||||||||| ||||||| |||||||||||||||||||||||||||||||||||
Db     978 AATGTCTGAATTGGAAAAACGAATTGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1037

Qy    1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
           |||||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||
Db    1038 TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC 1097

Qy    1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAA-----------ATTCTTCTTT 1125
           | | |||||||||||||||||| | ||  ||  |||           ||      ||
Db    1098 AAGTCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATT 1157

Qy    1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
           ||| |   |    || |||||||| || || || ||||| || || || || ||  | ||
Db    1158 GGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTC 1217

Qy    1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245
           |||||||  ||   || || ||| |  || | ||||| |    |    |||| |||||  |
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Db   1218 TCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT 1277

Qy   1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305
          | || || || ||| | || || |   ||   ||||| |||     |  |  |  || |
Db   1278 GGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAG 1337

Qy   1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365
          ||| | |||||||||  |||| || ||| |   |  || |       |||  |||  ||  |
Db   1338 TGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACT 1397

Qy   1366 TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 1425
          ||  ||||| |||||  |   ||||||  | || || || ||  | || |||||  | ||
Db   1398 TGATAATAAAGGTCGACAAGTTGATTTTGAGGCTTTGGATAACCTGTTGGAACGACTCAA 1457

Qy   1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
          ||||   | | | ||||||  || || || ||||||  |   | || ||| |||| || ||
Db   1458 GGATGTCCCAAGTGATAAAGTCAAGTTAGTGGATGATATTCTTGCCTTCTTAGCTCCGAT 1517

Qy   1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545
          |  |||||||| ||  | || |||||||||| | ||||||   || |||| || ||  |
Db   1518 TCGTCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGAT 1577

Qy   1546 TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA 1605
          ||   | ||  | || || |  ||||| |||||   ||| ||||| || ||||||   |
Db   1578 TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG 1637

Qy   1606 TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG 1665
          |||||||| ||||||||| || ||||| |||||||| || ||||||  ||||||| ||||
Db   1638 TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG 1697

Qy   1666 GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA 1725
          ||||  |||||||||  | |||||    || | ||  ||||| || || ||| |||||||
Db   1698 GATTAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGA 1757

Qy   1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785
          ||||||  |    ||||| ||  |||||    | | |  || |||| |    | | |  |
Db   1758 GAAAGGTTTGACCCCTCCTTCGACAGACCATCAGGATTCAGGAAATACTGAGGCAAAAGG 1817

Qy   1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845
          ||||  |||||  |||||  || |||||||  |  ||      | |||||  | |||  | ||
Db   1818 AGCAGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCC 1877

Qy   1846 ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA 1905
          ||  |   ||  |  |||| || || || ||||||||||  ||| || ||  |||||  | ||
Db   1878 TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA 1937

Qy   1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG 1965
          ||||||||||  || |||||||  |||||||| ||    |   ||  | || || || ||
Db   1938 CCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGG 1997

Qy   1966 CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG 2025
          |||||  | || ||| | || |||||  | ||||||||  || |||||  ||  |||||||
Db   1998 GTATACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG 2057

Qy   2026 TCCACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCA 2085
          ||| |||||  || |||| |  || || || || || |||||   | | || ||| |
Db   2058 TCCGCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGG 2117

Qy   2086 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGA---------------------- 2121
               |  ||| | ||| | |     ||| |    ||
Db   2118 TCAAGCTGATACCAATCAAACGGAAAAACCAAGCGAGGAGAAACCTCAGACAGAAAAACC 2177

Qy   2122 ------------------------------------------------------------ 2121

Db   2178 TGAGGAAGAAACCCCTCGAGAAGAGAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAACC 2237

Qy   2122 ---AGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAA 2178
             ||||  |  ||| ||| |||| |  ||  |||||  ||||| || ||||||||||
Db   2238 AACAGAGGAACCAGAAGAATCACCAGAGGAATCAGAAGAACCTCAGGTCGAGACTGAAAA 2297

Qy   2179 AGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCT 2238
          ||  ||||   |||| | ||| || |||| ||| ||||  |||  |   |||| | | | |
Db   2298 GGTTGAAGAAAAACTGAGAGAGGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTAT 2357

Qy   2239 GAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTAT 2298
          ||  ||||||| | ||| |||||  | || |||  |||||||||     ||   |
Db   2358 CAAGTCCAATGCCAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCA 2417

Qy   2299 GGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358
          ||| ||||||| ||| ||||||||||| |||||| || | || || ||||| |  |||||
Db   2418 GGACAACAATACTATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA 2477
```

RESULT 10
AAA47605
ID AAA47605 standard; DNA; 2531 BP.
XX
AC AAA47605;
XX
DT 20-OCT-2000 (first entry)
XX
DE Recombinant variant of Sp36 gene (Sp36B) of S. pneumoniae.
XX
KW Streptococcus pneumoniae; infection; vaccine; coiled coil region;
KW histidine triad residue; Sp36; antibody; otitis media;
KW nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
KW meningitis; lobar pneumonia; ds.
XX
OS Streptococcus pneumoniae.
XX
FH Key Location/Qualifiers
FT CDS 1..2531
FT /*tag= a
FT /product= Sp36B polypeptide
XX
PN WO200037105-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30390.
XX
PR 21-DEC-1998; 98US-0113048.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Johnson LS, Koenig S, Adamou JE;
XX
DR WPI; 2000-452129/39.
DR P-PSDB; AAB01469.
XX
PT Vaccine useful for prophylaxis and treatment of pnemococcal infections
PT such as otitis media, nasopharyngeal and bronchial infections,
PT comprises Streptococcus pneumoniae proteins
XX
PS Disclosure; Page 69-70; 70pp; English.
XX
CC Although a number of proteins have been suggested as being involved
CC in the pathogenicity of Streptococcus pneumoniae, there still remains
CC a need to identify polypeptides having epitopes in common from
CC various strains of S. pneumoniae in order to utilise such
CC polypeptides in vaccines to protect against a wide variety of
CC S. pneumoniae. New vaccine compositions are described which comprise a
CC Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
CC acids in length that comprise at least one histidine triad residue
CC (HxxHxH) or a coiled-coil region, or an antibody directed against
CC these features. The vaccine is useful in protecting against infection
CC by Streptococcus pneumoniae. The vaccine composition comprising
CC antibodies to is useful for passive immunization for treating
CC Pneumococcal infections which includes otitis media, nasopharyngeal
CC and bronchial infections.
XX
SQ Sequence 2531 BP; 861 A; 508 C; 550 G; 609 T; 3 other;

Query Match 41.5%; Score 991; DB 21; Length 2531;
Best Local Similarity 65.7%; Pred. No. 6.6e-239;
Matches 1609; Conservative 1; Mismatches 697; Indels 141; Gaps 6;

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Db   2169 CCCTCGAGAAGAGAAACCGCAAAGCGAGAAACCAGAGTCTCCAAAACCAACAGAGGAACC 2228

Qy   2131 AGAGGAAACACCTGCTGAGCCAGAAGTCCCTCAAGTAGAGACTGAAAAAGTAGAAGCCCA 2190

Db   2229 AGAAGAATCACCAGAGGAATCAGAAGAACCTCAGGTCGAGACTGAAAAGGTTGAAGAAAA 2288

Qy   2191 ACTCAAAGAAGCAGAAGTTTTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGCCAATGC 2250

Db   2289 ACTGAGAGAGGCTGAAGATTTACTTGGAAAAATCCAGGATCCAATTATCAAGTCCAATGC 2348

Qy   2251 AACAGAAACTCTAGCTGGTTTACGAAATAATTTGACTCTTCAAATTATGGATAACAATAG 2310

Db   2349 CAAAGAGACTCTCACAGGATTAAAAAATAATTTACTATTTGGCACCCAGGACAACAATAC 2408

Qy   2311 TATCATGGCAGAAGCAGAAAAATTACTTGCGTTGTTAAAAGGAAGTAA 2358

Db   2409 TATTATGGCAGAAGCTGAAAAACTATTGGCTTTATTAAAGGAGAGTAA 2456


RESULT 11
AAA47602
ID   AAA47602 standard; DNA; 2531 BP.
XX
AC   AAA47602;
XX
DT   20-OCT-2000  (first entry)
XX
DE   Recombinant variant of Sp36 gene (Sp36D) of S. pneumoniae.
XX
KW   Streptococcus pneumoniae; infection; vaccine; coiled coil region;
KW   histidine triad residue; Sp36; antibody; otitis media;
KW   nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
KW   meningitis; lobar pneumonia; ds.
XX
OS   Streptococcus pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..2517
FT                   /*tag= a
FT                   /product= Sp36D polypeptide
XX
PN   WO200037105-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30390.
XX
PR   21-DEC-1998;   98US-0113048.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Johnson LS,  Koenig S,  Adamou JE;
XX
DR   WPI; 2000-452129/39.
DR   P-PSDB; AAB01466.
XX
PT   Vaccine useful for prophylaxis and treatment of pnemococcal infections
PT   such as otitis media, nasopharyngeal and bronchial infections,
PT   comprises Streptococcus pneumoniae proteins
XX
PS   Disclosure; Page 57-58; 70pp; English.
XX
CC   Although a number of proteins have been suggested as being involved
CC   in the pathogenicity of Streptococcus pneumoniae, there still remains
CC   a need to identify polypeptides having epitopes in common from
CC   various strains of S. pneumoniae in order to utilise such
CC   polypeptides in vaccines to protect against a wide variety of
CC   S. pneumoniae. New vaccine compositions are described which comprise a
CC   Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino
CC   acids in length that comprise at least one histidine triad residue
CC   (HxxHxH) or a coiled-coil region, or an antibody directed against
CC   these features. The vaccine is useful in protecting against infection
CC   by Streptococcus pneumoniae. The vaccine composition comprising
CC   antibodies to is useful for passive immunization for treating
CC   Pneumococcal infections which includes otitis media, nasopharyngeal
CC   and bronchial infections.
XX
SQ   Sequence 2531 BP; 836 A; 511 C; 547 G; 637 T; 0 other;

  Query Match             41.4%;  Score 990;  DB 21;  Length 2531;
  Best Local Similarity   68.1%;  Pred. No. 1.2e-238;
  Matches 1478;  Conservative    0;  Mismatches  636;  Indels   57;  Gaps    5;

Qy      1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC 57

Db     60 TTCCTATGAACTTGGTCGTCACCAAGCTGGTCAGGTTAAGAAAGAGTCTAATCGAGTTTC 119

Qy     58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117

Db    120 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG 179

Qy    118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177

Db    180 TAAGAGGGAGGGGATCAACGCCGAACAAATCGTCATCAAGATTACGGATCAAGGTTATGT 239

Qy    178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237

Db    240 GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTCCCTTATGATGCCATCAT 299

Qy    238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297

Db    300 CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA 359

Qy    298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357

Db    360 TGAAATCAAGGGTGGTTATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 419

Qy    358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCA 417

Db    420 TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACA 479

Qy    418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477

Db    480 CAGTCATAATCACGGGGGTGGTTCT------AACGATCAAGCAGTAGTTGCAGCCAGAGC 533

Qy    478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537

Db    534 CCAAGGACGCTATACAACGGATGATGGTTATATCTTCAATGCATCTGATATCATTGAGGA 593

Qy    538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597

Db    594 CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA 653

Qy    598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657

Db    654 GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCT------------------------- 688

Qy    658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717

Db    689 --------ATTGGAATGGGAAGCAGGGATCTCGTCCTTCTTCAAGTTCTAGTTATAATGC 740

Qy    718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG 777

Db    741 AAATCCAGCTCAACCAAGATTGTCAGAGAACCACAATCTGACTGTCACTCCAACTTATCA 800

Qy    778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837

Db    801 TCA---AAATCAAGGGGAAAACATTTCAAGCCTTTTACGTGAATTGTATGCTAAACCCTT 857

Qy    838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897

Db    858 ATCAGAACGCCATGTGGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGTCG 917

Qy    898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957
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Db    918 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACA 977

Qy    958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017
          ||||||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db    978 AATGTCTGAATTGGAAAAACGAATTGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1037

Qy   1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
          ||||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||
Db   1038 TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC 1097

Qy   1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTC----------TTT 1125
          | | ||||||||||||||||||| | ||  ||   |||    | |           ||
Db   1098 AAGTCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATT 1157

Qy   1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
          ||| |   |    || |||||||| || || || ||||| || || || || ||  | ||
Db   1158 GGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTC 1217

Qy   1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245
          ||||||| ||   || || ||| |  || | ||||| |    |    |||| |||||  |
Db   1218 TCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT 1277

Qy   1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305
            | || || || ||| | || || |   ||   ||||| |||    |  |  |  || |
Db   1278 GGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAG 1337

Qy   1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365
          ||| | |||||||||  |||| || ||| |  |  || |      |||  |||  ||  |
Db   1338 TGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACT 1397

Qy   1366 TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 1425
          ||  ||||| |||||  |   ||||||  | || || || ||  | || |||||  | ||
Db   1398 TGATAATAAAGGTCGACAAGTTGATTTTGAGGCTTTGGATAACCTGTTGGAACGACTCAA 1457

Qy   1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
            ||||   | | | |||||  || || || ||||| |  | || ||| |||| || ||
Db   1458 GGATGTCCCAAGTGATAAAGTCAAGTTAGTGGATGATATTCTTGCCTTCTTAGCTCCGAT 1517

Qy   1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545
          |  |||||||| ||  | || ||||||||| | ||||||   || ||||| || ||  |
Db   1518 TCGTCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGAT 1577

Qy   1546 TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA 1605
          ||   | ||  | || || |  ||||| |||||   ||| ||||| || ||||||   |
Db   1578 TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG 1637

Qy   1606 TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG 1665
          |||||||| ||||||||| || ||||| |||||||| || ||||||  ||||||  |||||
Db   1638 TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG 1697

Qy   1666 GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA 1725
          ||||  |||||||||  | |||||    || | ||  ||||| || || ||| |||||||
Db   1698 GATTAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGA 1757

Qy   1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785
          ||||||  |    ||||| ||  |||||    | | |  || |||| |    | | |  |
Db   1758 GAAAGGTTTGACCCCTCCTTCGACAGACCATCAGGATTCAGGAAATACTGAGGCAAAAGG 1817

Qy   1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845
          |||| |||||| ||||| || |||||||  |  ||     | ||||| | |||  | ||
Db   1818 AGCAGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCC 1877

Qy   1846 ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA 1905
            || |   || |  |||| || || || ||||||||| ||| || || |||||| | ||
Db   1878 TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA 1937

Qy   1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG 1965
          ||||||||||| || ||||||| |||||||| ||   |   ||  | || || || ||
Db   1938 CCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGG 1997

Qy   1966 CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG 2025
          |||||  | || ||| | || |||||  | |||||||| || ||||| ||  |||||||
Db   1998 GTATACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG 2057

Qy   2026 TCCACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCA 2085
          ||| |||||  || |||| |  || || || || || |||||       || || |   |
Db   2058 TCCGCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCGTAAAAATAAGGTAGA 2117

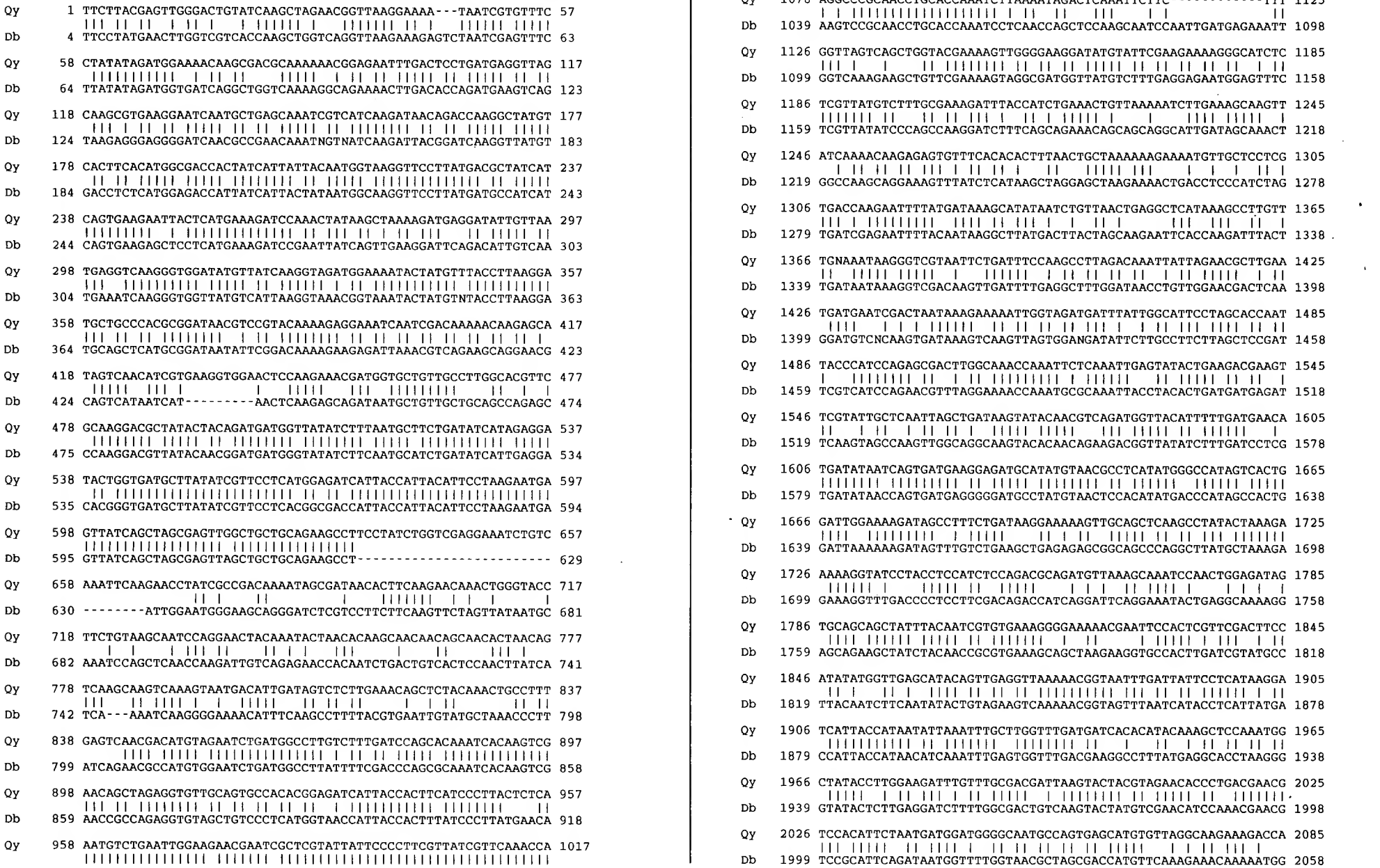
Qy   2086 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGC 2145
          |   ||   |  | | |  |    || |   |||| ||   |   |||  ||| |   |
Db   2118 CCAAGACAGTAAACCTGATGAAGATAAGGAACATGATGAAGTAAGTGAGCCAACTCACCC 2177

Qy   2146 TGAGCCAGAAG 2156
          |||  | || |
Db   2178 TGAATCTGATG 2188
```

RESULT 12
AAV27356
ID AAV27356 standard; DNA; 2290 BP.
XX
AC AAV27356;
XX
DT 02-OCT-1998 (first entry)
XX
DE Streptococcus pneumoniae SP0042 nucleotide.
XX
KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
KW detection; pneumonia; otitis media; meningitis; ss.
XX
OS Streptococcus pneumoniae.
XX
FH Key   Location/Qualifiers
FT CDS   2..2290
FT   /*tag= a
FT   /product= "SP0042"
FT   /transl_except= (pos:152..154,aa:Xaa)
FT   /transl_except= (pos:1406..1408,aa:Xaa)
FT   /transl_except= (pos:1430..1432,aa:Xaa)
FT   /note= "no stop codon given; Xaa is unspecified"
XX
PN WO9818930-A2.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US19422.
XX
PR 31-OCT-1996; 96US-0029960.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
XX
DR WPI; 1998-272224/24.
DR P-PSDB; AAW55095.
XX
PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
PT pneumoniae - or their epitope-containing fragments, useful in
PT protective or therapeutic vaccines, and for diagnosis
XX
PS Claim 1; Page 61-62; 118pp; English.
XX
CC The present sequence encodes a protein from Streptococcus pneumoniae.
CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
CC can be useful in vaccines for inducing protective antibodies against
CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
CC are used to detect Streptococcus infection (by usual hybridisation or
CC amplification methods), also for isolating Streptococcus genes or their
CC allelic variants. The protein can be used similarly to detect specific
CC antibodies in standard immunoassays, especially for diagnosing or
CC monitoring infections. Antibodies which bind the protein are used to
CC detect corresponding antigens, to purify the protein and for passive
CC immunisation (optionally coupled to a toxin). Vaccines are administered,
CC e.g. by injection, orally or through the skin, typically at 0.01-1000
CC (especially 10-300) mu g/ml per dose.

XX
SQ Sequence 2290 BP; 766 A; 474 C; 498 G; 547 T; 5 other;

Query Match 41.3%; Score 987.6; DB 19; Length 2290;
Best Local Similarity 67.7%; Pred. No. 4.5e-238;
Matches 1481; Conservative 0; Mismatches 645; Indels 60; Gaps 5;



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Qy   2086 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGC 2145
Db   2059 TCAAGCTGATACCAATCAAACGGAAAAACCAAGCGAGGAGAAACCTCAGACAGAAAAACC 2118

Qy   2146 TGAGCCAGAAGTCCCTCAAGTAGAGA 2171
Db   2119 TGAGGAAGAAACCCCTCGAGAAGAGA 2144
```

RESULT 13
ABQ84824
ID ABQ84824 standard; DNA; 2290 BP.
XX
AC ABQ84824;
XX
DT 04-SEP-2002 (first entry)
XX
DE S. pneumoniae SP042 nucleotide sequence SEQ ID NO:65.
XX
KW Streptococcus pneumoniae; epitope; vaccine; antigenic protein;
KW antibacterial; Streptococcal infection; detection; gene; ds.
XX
OS Streptococcus pneumoniae.
XX
PN US2002061545-A1.
XX
PD 23-MAY-2002.
XX
PF 22-JAN-2001; 2001US-0765272.
XX
PR 30-OCT-1997; 97US-0961083.
XX
PA (CHOI/) CHOI G H.
PA (KUNS/) KUNSCH C A.
PA (BARA/) BARASH S C.
PA (DILL/) DILLON P J.
PA (DOUG/) DOUGHERTY B.
PA (FANN/) FANNON M R.
PA (ROSE/) ROSEN C A.
XX
PI Choi GH, Kunsch CA, Barash SC, Dillon PJ, Dougherty B, Fannon MR;
PI Rosen CA;
XX
DR WPI; 2002-479261/51.
DR P-PSDB; ABP54589.
XX
PT New Streptococcus pneumoniae antigens, useful for detecting
PT Streptococcus and for preventing or attenuating disease caused by
PT Streptococcus infection -
XX
PS Claim 1; Page 28-29; 70pp; English.
XX
CC ABQ84792 to ABQ84904 represents nucleic acids which encode the
CC Streptococcus pneumoniae antigens given in ABP54557 to ABP54669.
CC The S. pneumoniae antigens have antibacterial activity and can be
CC used in vaccines. The S. pneumoniae antigens can also be used to
CC prevent or attenuate a Streptococcal infection in an animal. The
CC polynucleotides encoding the S. pneumoniae antigens can be used to
CC detect Streptococcus nucleic acids. ABQ84905 to ABQ85130 represent
CC primers used in the cloning of S. pneumoniae ORFs (open reading frames)
CC which are used in an example from the present invention.
XX
SQ Sequence 2290 BP; 766 A; 474 C; 498 G; 547 T; 5 other;

```
  Query Match            41.3%;  Score 987.6;  DB 24;  Length 2290;
  Best Local Similarity  67.7%;  Pred. No. 4.5e-238;
  Matches 1481;  Conservative    0;  Mismatches  645;  Indels   60;  Gaps    5;

Qy       1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC 57
Db       4 TTCCTATGAACTTGGTCGTCACCAAGCTGGTCAGGTTAAGAAAGAGTCTAATCGAGTTTC 63

Qy      58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117
Db      64 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAACTTGACACCAGATGAAGTCAG 123

Qy     118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
Db     124 TAAGAGGGAGGGGATCAACGCCGAACAAATNGTNATCAAGATTACGGATCAAGGTTATGT 183

Qy     178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237
Db     184 GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT 243

Qy     238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297
Db     244 CAGTGAAGAGCTCCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA 303

Qy     298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
Db     304 TGAAATCAAGGGTGGTTATGTCATTAAGGTAAACGGTAAATACTATGTNTACCTTAAGGA 363

Qy     358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCA 417
Db     364 TGCAGCTCATGCGGATAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACG 423

Qy     418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477
Db     424 CAGTCATAATCAT---------AACTCAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC 474

Qy     478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
Db     475 CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA 534

Qy     538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
Db     535 CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA 594

Qy     598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657
Db     595 GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCT------------------------- 629

Qy     658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717
Db     630 --------ATTGGAATGGGAAGCAGGGATCTCGTCCTTCTTCAAGTTCTAGTTATAATGC 681

Qy     718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG 777
Db     682 AAATCCAGCTCAACCAAGATTGTCAGAGAACCACAATCTGACTGTCACTCCAACTTATCA 741

Qy     778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837
Db     742 TCA---AAATCAAGGGGAAAACATTTCAAGCCTTTTACGTGAATTGTATGCTAAACCCTT 798

Qy     838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897
Db     799 ATCAGAACGCCATGTGGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGTCG 858

Qy     898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957
Db     859 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACA 918

Qy     958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017
Db     919 AATGTCTGAATTGGAAAAACGAATTGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 978

Qy    1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
Db     979 TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC 1038

Qy    1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTC------------TTT 1125
Db    1039 AAGTCCGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATT 1098

Qy    1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
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Db  1099 GGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTC 1158

Qy  1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245

Db  1159 TCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT 1218

Qy  1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305

Db  1219 GGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAG 1278

Qy  1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365

Db  1279 TGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACT 1338

Qy  1366 TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 1425

Db  1339 TGATAATAAAGGTCGACAAGTTGATTTTGAGGCTTTGGATAACCTGTTGGAACGACTCAA 1398

Qy  1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485

Db  1399 GGATGTCNCAAGTGATAAAGTCAAGTTAGTGGANGATATTCTTGCCTTCTTAGCTCCGAT 1458

Qy  1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545

Db  1459 TCGTCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGAT 1518

Qy  1546 TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA 1605

Db  1519 TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG 1578

Qy  1606 TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG 1665

Db  1579 TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG 1638

Qy  1666 GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA 1725

Db  1639 GATTAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGA 1698

Qy  1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785

Db  1699 GAAAGGTTTGACCCCTCCTTCGACAGACCATCAGGATTCAGGAAATACTGAGGCAAAAGG 1758

Qy  1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845

Db  1759 AGCAGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCC 1818

Qy  1846 ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA 1905

Db  1819 TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA 1878

Qy  1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG 1965

Db  1879 CCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGG 1938

Qy  1966 CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG 2025

Db  1939 GTATACTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG 1998

Qy  2026 TCCACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCA 2085

Db  1999 TCCGCATTCAGATAATGGTTTTGGTAACGCTAGCGACCATGTTCAAAGAAACAAAAATGG 2058

Qy  2086 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGC 2145

Db  2059 TCAAGCTGATACCAATCAAACGGAAAAACCAAGCGAGGAGAAACCTCAGACAGAAAAACC 2118

Qy  2146 TGAGCCAGAAGTCCCTCAAGTAGAGA 2171

Db  2119 TGAGGAAGAAACCCCTCGAGAAGAGA 2144

RESULT 14
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AAA65737
ID   AAA65737 standard; DNA; 2639 BP.
XX
AC   AAA65737;
XX
DT   21-NOV-2000  (first entry)
XX
DE   Streptococcus pneumoniae BVH-11-2 gene SEQ ID NO:13.
XX
KW   Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW   prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW   otitis media; pneumonia; immunisation; bactericidal; ds.
XX
OS   Streptococcus pneumoniae.
XX
PN   WO200039299-A2.
XX
PD   06-JUL-2000.
XX
PF   20-DEC-1999;   99WO-CA01218.
XX
PR   23-DEC-1998;   98US-0113800.
XX
PA   (BIOC-) BIOCHEM PHARMA INC.
XX
PI   Hamel J,  Brodeur BR,  Pineau I,  Martin D,  Rioux C,  Charland N;
XX
DR   WPI; 2000-452397/39.
DR   P-PSDB; AAB12720.
XX
PT   Streptococcal antigens useful for vaccinating against e.g. meningitis,
PT   otitis media, bacteremia and/or pneumonia -
XX
PS   Example 6; Fig 16; 106pp; English.
XX
CC   The present invention describes nucleic acids (I) encoding protein
CC   antigens (II) from Streptococcus pneumoniae. The protein antigens
CC   have bactericidal activity. The nucleic acids, encoding the protein
CC   antigens, may be used for the recombinant production of the proteins
CC   they encode. The protein antigens may then be used as vaccines for the
CC   prevention and treatment of Streptococcal infections in mammals
CC   (especially humans) which result in, e.g. meningitis, otitis media,
CC   bacteraemia and/or pneumonia. The present sequence encodes the
CC   S. pneumoniae BVH-11-2 protein antigen.
XX
SQ   Sequence 2639 BP; 889 A; 518 C; 567 G; 665 T; 0 other;

  Query Match             41.1%;  Score 980.8;  DB 21;  Length 2639;
  Best Local Similarity   67.8%;  Pred. No. 2.5e-236;
  Matches 1473;  Conservative    0;  Mismatches  638;  Indels   60;  Gaps    5;

Qy       1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC 57

Db     173 TTCCTATGAACTTGGTCGTCACCAAGCTGGTCAGGTTAAGAAAGAGTCTAATCGAGTTTC 232

Qy      58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117

Db     233 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAATTTGACACCAGATGAAGTCAG 292

Qy     118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177

Db     293 TAAGAGAGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT 352

Qy     178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237

Db     353 GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT 412

Qy     238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297

Db     413 CAGTGAAGAACTTCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA 472

Qy     298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
```

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Db    473 TGAAATCAAGGGTGGCTATGTGATTAAGGTAGACGGAAAATACTATGTTTACCTTAAAGA 532

Qy    358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCA 417
          ||| ||||| ||||| || | || |||||||| || || || || || || || || ||
Db    533 TGCGGCCCATGCGGACAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACA 592

Qy    418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477
          |||||  ||| |         |   |||||   |||  |||||||||     ||  |  |
Db    593 CAGTCATAATCAT---------AACTCAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC 643

Qy    478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
          ||||||||| |||||  || |||||||| ||||||||  ||||| ||||||||||| ||||||
Db    644 CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA 703

Qy    538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
          || ||||||||||||||||||||||| || || ||||||||||||||||||||||||||||
Db    704 CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA 763

Qy    598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657
          ||||||||||||||||| |||||||||||||||
Db    764 GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCT------------------------ 798

Qy    658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717
                    || |    ||          |    |||||||  | |  |       |
Db    799 --------ATTGGAATGGGAAGCAGGGATCTCGTCCTTCTTCAAGTTCTAGTTATAATGC 850

Qy    718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG 777
            |  |    | ||| ||    || | |   |||      |    ||      ||| |
Db    851 AAATCCAGTTCAACCAAGATTGTCAGAGAACCACAATCTGACTGTCACTCCAACTTATCA 910

Qy    778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837
          |||   || |||| |   |  |||||   || || ||     |  ||      || ||
Db    911 TCA---AAATCAAGGGGAAAACATTTCAAGCCTTTTACGTGAATTGTATGCTAAACCCTT 967

Qy    838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897
              |||| |||||||||||||||||||||| | || || ||||| ||||||||||||||
Db    968 ATCAGAACGCCATGTAGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGTCG 1027

Qy    898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957
          ||| || |||||||| || || || || ||   | ||||||||||| ||||||||     ||
Db   1028 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACA 1087

Qy    958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017
          |||||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||||
Db   1088 AATGTCTGAATTGGAAAAACGAATTGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1147

Qy   1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
          |||||||||||||||||| ||||||||||||||||||| ||||||||||||||||||||
Db   1148 TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC 1207

Qy   1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTC------------TTT 1125
          | | | |||||||||||||||||| | ||  ||   |||     | |             ||
Db   1208 AAGTCTGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATT 1267

Qy   1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
          |||  |   |    || |||||||| || || || ||||| || || || || ||  | ||
Db   1268 GGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTC 1327

Qy   1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245
          |||||||  ||   || || ||| |  || | ||||| |     |    |||| |||||  |
Db   1328 TCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT 1387

Qy   1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305
            | || || || ||| | || || |   ||   ||||| |||    |  |  |  || |
Db   1388 GGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAG 1447

Qy   1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365
          ||| | |||||||||  |||| || ||| |  |  || |      |||  |||  ||  |
Db   1448 TGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACT 1507

Qy   1366 TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 1425
          ||  ||||| |||||  |   ||||||  | |  || || ||  | || |||||  | ||
Db   1508 TGATAATAAAGGTCGACAAGTTGATTTTGAGGTTTTGGATAACCTGTTGGAACGACTCAA 1567
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Qy   1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485
          ||||  || | | ||||||  || || || |||||| |  | || ||| |||| || ||
Db   1568 GGATGTCTCAAGTGATAAAGTCAAGTTAGTGGATGATATTCTTGCCTTCTTAGCTCCGAT 1627

Qy   1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545
          |   |||||||| ||  | || |||||||| | ||||||   || ||||| || ||  |
Db   1628 TCGTCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGAT 1687

Qy   1546 TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA 1605
          ||   | ||  | || || |  ||||| |||||   ||| ||||| || ||||||   |
Db   1688 TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG 1747

Qy   1606 TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG 1665
          |||||||| ||||||||| || ||||| |||||||| || ||||||  ||||||| |||||
Db   1748 TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG 1807

Qy   1666 GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA 1725
          ||||  |||||||||  | |||||     || | ||  ||||| || || ||| |||||||
Db   1808 GATTAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGA 1867

Qy   1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785
          ||||||  |    ||||| ||  |||||     | | |  || |||| |    | | |  |
Db   1868 GAAAGGTTTGACCCCTCCTTCGACAGACCACCAGGATTCAGGAAATACTGAGGCAAAAGG 1927

Qy   1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845
          ||||  |||||| ||||| || |||||||  |  ||      | |||||  | |||  | ||
Db   1928 AGCAGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCC 1987

Qy   1846 ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA 1905
          || |   || |  |||| || || || ||||||||||  ||| || || ||||||  | ||
Db   1988 TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA 2047

Qy   1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG 1965
          ||||||||||| || |||||||  |||||||| ||    |   ||  | || || || ||
Db   2048 CCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGG 2107

Qy   1966 CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG 2025
          ||||   | || ||| | || |||||  | |||||||| || ||||| ||  |||||||
Db   2108 GTATAGTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG 2167

Qy   2026 TCCACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCA 2085
          ||| |||||  || |||| |  || || || ||||| |||||        || || |   |
Db   2168 TCCGCATTCAGATAATGGTTTTGGTAACGCTAGTGACCATGTTCGTAAAAATAAGGCAGA 2227

Qy   2086 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGC 2145
          |   ||   |  |  | |  |    || |   |||| ||   |   |||  ||| |   |
Db   2228 CCAAGATAGTAAACCTGATGAAGATAAGGAACATGATGAAGTAAGTGAGCCAACTCACCC 2287

Qy   2146 TGAGCCAGAAG 2156
          |||  | || |
Db   2288 TGAATCTGATG 2298
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RESULT 15
ABK15104
ID   ABK15104 standard; DNA; 2639 BP.
XX
AC   ABK15104;
XX
DT   08-MAY-2002  (first entry)
XX
DE   DNA encoding Streptococcus pneumoniae BVH-11-2.
XX
KW   BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia;
KW   pneumonia; streptococcal bacterial infection; gene; ds; BVH-11-2.
XX
OS   Streptococcus pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             114..2630
FT                   /*tag= a
FT                   /product= "BVH-11-2"
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FT                   /note= "The gene is flanked by sequences from the
FT                          vector SP64, no information on which is
FT                          given in the specification"
XX
PN   WO200198334-A2.
XX
PD   27-DEC-2001.
XX
PF   19-JUN-2001; 2001WO-CA00908.
XX
PR   20-JUN-2000; 2000US-212683P.
XX
PA   (SHIR-) SHIRE BIOCHEM INC.
XX
PI   Hamel J,  Ouellet C,  Charland N,  Martin D,  Brodeur B;
XX
DR   WPI; 2002-122272/16.
DR   P-PSDB; AAU75934.
XX
PT   New Streptococcus pneumoniae BVH-3 and BVH-11 variant and
PT   epitope-bearing polypeptides, useful as vaccine components for treating
PT   or preventing streptococcal infections such as otitis media,
PT   meningitis, and bacteraemia  -
XX
PS   Example 3; Fig 5; 113pp; English.
XX
CC   The invention describes an isolated polypeptide (I) with 70-90%
CC   identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of
CC   BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II)
CC   comprising (I) is useful for therapeutic or prophylactic treatment of
CC   meningitis, otitis media, bacteraemia or pneumonia infection in an
CC   individual susceptible to these disorders. (II) is also useful for
CC   therapeutic or prophylactic treatment of any streptococcal bacterial
CC   infection (e.g., caused by Streptococcus pneumoniae, group A
CC   Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
CC   as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or
CC   Staphylococcus aureus) in an individual susceptible to the infection.
CC   A polynucleotide (III) encoding (I) is useful in DNA immunisation
CC   techniques. The Streptococcus polypeptides are useful in a diagnostic
CC   test for S. pneumoniae infection. (III) is useful for designing DNA
CC   probes for use in detecting the presence of Streptococcus in a biological
CC   sample suspected of containing the bacteria. The DNA probes may also be
CC   used for detecting circulating S. pneumonia nucleic acid in a sample for
CC   diagnosing streptococcal infections. This sequence encodes the
CC   Streptococcus pneumoniae protein BVH-11-2, used to create the antigenic
CC   peptides described in the method of the invention.
XX
SQ   Sequence 2639 BP; 889 A; 518 C; 567 G; 665 T; 0 other;

  Query Match             41.1%;  Score 980.8;  DB 24;  Length 2639;
  Best Local Similarity   67.8%;  Pred. No. 2.5e-236;
  Matches 1473;  Conservative    0;  Mismatches  638;  Indels   60;  Gaps    5;

Qy       1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAA---TAATCGTGTTTC 57
Db     173 TTCCTATGAACTTGGTCGTCACCAAGCTGGTCAGGTTAAGAAAGAGTCTAATCGAGTTTC 232

Qy      58 CTATATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAG 117
Db     233 TTATATAGATGGTGATCAGGCTGGTCAAAAGGCAGAAAATTTGACACCAGATGAAGTCAG 292

Qy     118 CAAGCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGT 177
Db     293 TAAGAGAGAGGGGATCAACGCCGAACAAATTGTTATCAAGATTACGGATCAAGGTTATGT 352

Qy     178 CACTTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCAT 237
Db     353 GACCTCTCATGGAGACCATTATCATTACTATAATGGCAAGGTTCCTTATGATGCCATCAT 412

Qy     238 CAGTGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAA 297
Db     413 CAGTGAAGAACTTCTCATGAAAGATCCGAATTATCAGTTGAAGGATTCAGACATTGTCAA 472

Qy     298 TGAGGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGA 357
Db     473 TGAAATCAAGGGTGGCTATGTGATTAAGGTAGACGGAAAATACTATGTTTACCTTAAAGA 532

Qy     358 TGCTGCCCACGCGGATAACGTCCGTACAAAAGAGGAAATCAATCGACAAAAACAAGAGCA 417
Db     533 TGCGGCCCATGCGGACAATATTCGGACAAAAGAAGAGATTAAACGTCAGAAGCAGGAACA 592

Qy     418 TAGTCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTC 477
Db     593 CAGTCATAATCAT---------AACTCAAGAGCAGATAATGCTGTTGCTGCAGCCAGAGC 643

Qy     478 GCAAGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGA 537
Db     644 CCAAGGACGTTATACAACGGATGATGGGTATATCTTCAATGCATCTGATATCATTGAGGA 703

Qy     538 TACTGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGA 597
Db     704 CACGGGTGATGCTTATATCGTTCCTCACGGCGACCATTACCATTACATTCCTAAGAATGA 763

Qy     598 GTTATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTC 657
Db     764 GTTATCAGCTAGCGAGTTAGCTGCTGCAGAAGCCT---------------------------- 798

Qy     658 AAATTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACC 717
Db     799 --------ATTGGAATGGGAAGCAGGGATCTCGTCCTTCTTCAAGTTCTAGTTATAATGC 850

Qy     718 TTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGCAACACTAACAG 777
Db     851 AAATCCAGTTCAACCAAGATTGTCAGAGAACCACAATCTGACTGTCACTCCAACTTATCA 910

Qy     778 TCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTT 837
Db     911 TCA---AAATCAAGGGGAAAACATTTCAAGCCTTTTACGTGAATTGTATGCTAAACCCTT 967

Qy     838 GAGTCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCG 897
Db     968 ATCAGAACGCCATGTAGAATCTGATGGCCTTATTTTCGACCCAGCGCAAATCACAAGTCG 1027

Qy     898 AACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCA 957
Db    1028 AACCGCCAGAGGTGTAGCTGTCCCTCATGGTAACCATTACCACTTTATCCCTTATGAACA 1087

Qy     958 AATGTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1017
Db    1088 AATGTCTGAATTGGAAAAACGAATTGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCA 1147

Qy    1018 TTGGGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCC 1077
Db    1148 TTGGGTACCAGATTCAAGACCAGAACAACCAAGTCCACAATCGACTCCGGAACCTAGTCC 1207

Qy    1078 AGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTC------------TTT 1125
Db    1208 AAGTCTGCAACCTGCACCAAATCCTCAACCAGCTCCAAGCAATCCAATTGATGAGAAATT 1267

Qy    1126 GGTTAGTCAGCTGGTACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTC 1185
Db    1268 GGTCAAAGAAGCTGTTCGAAAAGTAGGCGATGGTTATGTCTTTGAGGAGAATGGAGTTTC 1327

Qy    1186 TCGTTATGTCTTTGCGAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTT 1245
Db    1328 TCGTTATATCCCAGCCAAGGATCTTTCAGCAGAAACAGCAGCAGGCATTGATAGCAAACT 1387

Qy    1246 ATCAAAACAAGAGAGTGTTTCACACACTTTAACTGCTAAAAAAGAAAATGTTGCTCCTCG 1305
Db    1388 GGCCAAGCAGGAAAGTTTATCTCATAAGCTAGGAGCTAAGAAAACTGACCTCCCATCTAG 1447

Qy    1306 TGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTT 1365
Db    1448 TGATCGAGAATTTTACAATAAGGCTTATGACTTACTAGCAAGAATTCACCAAGATTTACT 1507

Qy    1366 TGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAA 1425
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Db    1508 TGATAATAAAGGTCGACAAGTTGATTTTGAGGTTTTGGATAACCTGTTGGAACGACTCAA 1567

Qy    1426 TGATGAATCGACTAATAAAGAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAAT 1485

Db    1568 GGATGTCTCAAGTGATAAAGTCAAGTTAGTGGATGATATTCTTGCCTTCTTAGCTCCGAT 1627

Qy    1486 TACCCATCCAGAGCGACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGT 1545

Db    1628 TCGTCATCCAGAACGTTTAGGAAAACCAAATGCGCAAATTACCTACACTGATGATGAGAT 1687

Qy    1546 TCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACA 1605

Db    1688 TCAAGTAGCCAAGTTGGCAGGCAAGTACACAACAGAAGACGGTTATATCTTTGATCCTCG 1747

Qy    1606 TGATATAATCAGTGATGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTG 1665

Db    1748 TGATATAACCAGTGATGAGGGGGATGCCTATGTAACTCCACATATGACCCATAGCCACTG 1807

Qy    1666 GATTGGAAAAGATAGCCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGA 1725

Db    1808 GATTAAAAAAGATAGTTTGTCTGAAGCTGAGAGAGCGGCAGCCCAGGCTTATGCTAAAGA 1867

Qy    1726 AAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAG 1785

Db    1868 GAAAGGTTTGACCCCTCCTTCGACAGACCACCAGGATTCAGGAAATACTGAGGCAAAAGG 1927

Qy    1786 TGCAGCAGCTATTTACAATCGTGTGAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCC 1845

Db    1928 AGCAGAAGCTATCTACAACCGCGTGAAAGCAGCTAAGAAGGTGCCACTTGATCGTATGCC 1987

Qy    1846 ATATATGGTTGAGCATACAGTTGAGGTTAAAAACGGTAATTTGATTATTCCTCATAAGGA 1905

Db    1988 TTACAATCTTCAATATACTGTAGAAGTCAAAAACGGTAGTTTAATCATACCTCATTATGA 2047

Qy    1906 TCATTACCATAATATTAAATTTGCTTGGTTTGATGATCACACATACAAAGCTCCAAATGG 1965

Db    2048 CCATTACCATAACATCAAATTTGAGTGGTTTGACGAAGGCCTTTATGAGGCACCTAAGGG 2107

Qy    1966 CTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACG 2025

Db    2108 GTATAGTCTTGAGGATCTTTTGGCGACTGTCAAGTACTATGTCGAACATCCAAACGAACG 2167

Qy    2026 TCCACATTCTAATGATGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGACCA 2085

Db    2168 TCCGCATTCAGATAATGGTTTTGGTAACGCTAGTGACCATGTTCGTAAAAATAAGGCAGA 2227

Qy    2086 CAGTGAAGATCCAAATAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGC 2145

Db    2228. CCAAGATAGTAAACCTGATGAAGATAAGGAACATGATGAAGTAAGTGAGCCAACTCACCC 2287

Qy    2146 TGAGCCAGAAG 2156

Db    2288 TGAATCTGATG 2298


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